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(54) Title: POLYNUCLEOTIDES, POLYPEPTIDES EXPRESSED BY THE POLYNUCLEOTIDES AND METHODS FOR  
THEIR USE

(57) Abstract: Novel polynucleotides including partial and extended sequences, and open reading frames, are provided, together  
with probes and primers, DNA constructs comprising the polynucleotides, biological materials and organisms incorporating the  
polynucleotides, polypeptides expressed by the polynucleotides, and methods for using the polynucleotides and polypeptides.

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## POLYNUCLEOTIDES, POLYPEPTIDES EXPRESSED BY THE POLYNUCLEOTIDES AND METHODS FOR THEIR USE

### 5 Technical Field of the Invention

This invention relates to polynucleotides believed to be novel, including partial, extended and full length sequences, as well as probes and primers, genetic constructs comprising the polynucleotides, biological materials incorporating the polynucleotides, polypeptides expressed by the polynucleotides, and methods for  
10 using the polynucleotides and polypeptides.

### Background of the Invention

Sequencing of the genomes, or portions of the genomes, of numerous biological materials, including humans, animals, microorganisms and various  
15 plant varieties, has been and is being carried out on a large scale. Polynucleotides identified using sequencing techniques may be partial or full-length genes, and may contain open reading frames, or portions of open reading frames, that encode polypeptides. Putative polypeptides may be determined based on polynucleotide sequences. The sequencing data relating to polynucleotides thus represents  
20 valuable and useful information.

Polynucleotides may be analyzed for various degrees of novelty by comparing identified sequences to sequences published in various public domain databases, such as EMBL. Newly identified polynucleotides and putative polypeptides may also be compared to polynucleotides and polypeptides  
25 contained in public domain information to ascertain homology to known polynucleotides and polypeptides. In this way, the degree of similarity, identity or homology of polynucleotides and polypeptides of unknown function may be determined relative to polynucleotides and polypeptides having known functions.

Information relating to the sequences of isolated polynucleotides may be  
30 used in a variety of ways. Specified polynucleotides having a particular sequence may be isolated, or synthesized, for use in *in vivo* or *in vitro* experimentation as

probes or primers. Alternatively, collections of sequences of isolated polynucleotides may be stored using magnetic or optical storage medium, and analyzed or manipulated using computer hardware and software, as well as other types of tools.

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### Summary of the Invention

The present invention relates to polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NOS: 1-35, variants of those sequences, extended sequences comprising the sequences set out in SEQ ID NOS: 1-35 and  
10 their variants, probes and primers corresponding to the sequences set out in SEQ ID NOS: 1-35 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of the polynucleotides identified as SEQ ID NOS: 1-35 (x-mers), and extended sequences comprising portions of the sequences set out in SEQ ID NOS: 1-35, all of which are referred to herein,  
15 collectively, as “polynucleotides of the present invention.”

The polynucleotide sequences identified as SEQ ID NOS: 1-35 were derived from mammalian sources, namely, from mouse airways induced eosinophilia, rat dermal papilla and mouse stromal cells. Some of the polynucleotides of the present invention are “partial” sequences, in that they do  
20 not represent a full-length gene encoding a full-length polypeptide. Such partial sequences may be extended by further analyzing and sequencing the EST clones from which the sequences were obtained, or by analyzing and sequencing various DNA libraries (e.g. cDNA or genomic) using primers and/or probes and well known hybridization and/or PCR techniques. The partial sequences identified as  
25 SEQ ID NOS: 1-35 may thus be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as  
“corresponding to” a sequence identified as one of the sequences of SEQ ID NOS:  
30 1-35 or a variant thereof, or a portion of one of the sequences of SEQ ID NOS: 1-35 or a variant thereof, when the extended polynucleotide comprises an identified

sequence or its variant, or an identified contiguous portion (x-mer) of one of the sequences of SEQ ID NOS: 1-35 or a variant thereof.

The polynucleotides identified as SEQ ID NOS: 1-35 were isolated from mouse and rat cDNA clones and represent sequences that are expressed in the tissue from which the cDNA was prepared. The sequence information may be used to isolate or synthesize expressible DNA molecules, such as open reading frames or full-length genes, that can then be used as expressible or otherwise functional DNA in transgenic mammals and other organisms. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NOS: 1-35.

In a first aspect, the present invention provides isolated polynucleotide sequences comprising a polynucleotide selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-35; (b) complements of the sequences recited in SEQ ID NO: 1-35; (c) reverse complements of the sequences recited in SEQ ID NO: 1-35; (d) reverse sequences of the sequences recited in SEQ ID NO: 1-35; (e) sequences having either 40%, 60%, 75% or 90% identical nucleotides, as defined herein, to a sequence of (a) – (d); probes and primers corresponding to the sequences set out in SEQ ID NO: 1-35; polynucleotides comprising at least a specified number of contiguous residues of any of the polynucleotides identified as SEQ ID NO: 1-35; and extended sequences comprising portions of the sequences set out in SEQ ID NO: 1-35; all of which are referred to herein as “polynucleotides of the present invention”. The present invention also provides isolated polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 36-65; polypeptide variants of those sequences; and polypeptides comprising the isolated polypeptide sequences and variants of those sequences.

In another aspect, the present invention provides genetic constructs comprising a polynucleotide of the present invention, either alone, or in combination with one or more additional polynucleotides of the present invention,



or in combination with one or more known polynucleotides, together with cells and target organisms comprising such constructs.

The polynucleotides identified as SEQ ID NOS: 1-35 may contain open reading frames ("ORFs") or partial open reading frames encoding polypeptides. Additionally, open reading frames encoding polypeptides may be identified in extended or full-length sequences corresponding to the sequences set out as SEQ ID NOS: 1-35. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are available, for example, on the Internet at <http://www.ncbi.nlm.nih.gov/gorf/gorf.html>. Open reading frames and portions of open reading frames may be identified in the polynucleotides of the present invention. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified. Thus, polynucleotides and open reading frames encoding polypeptides may be identified using the polynucleotides of the present invention.

Once open reading frames are identified in the polynucleotides of the present invention, the open reading frames may be isolated and/or synthesized. Expressible DNA constructs may then be constructed that comprise the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art. Such DNA constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells.

Polypeptides encoded by the polynucleotides of the present invention may be expressed and used in various assays to determine their biological activity. Such polypeptides may be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

In another aspect, the present invention provides isolated polypeptides encoded, or partially encoded, by the above polynucleotides. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term "polypeptide encoded by a polynucleotide" as used herein, includes polypeptides encoded by a polynucleotide that comprises an isolated polynucleotide sequence or variant provided herein. Polypeptides of the present invention may be naturally purified products, or may be produced partially or wholly using recombinant techniques. Such polypeptides may be glycosylated with bacterial, fungal, mammalian or other eukaryotic carbohydrates or may be non-glycosylated. In specific embodiments, the inventive polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 36-65.

Polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide sequence that encodes the polypeptide into a genetic construct and expressing the polypeptide in an appropriate host. Any of a variety of genetic constructs known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with a genetic construct containing a polynucleotide that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are *Escherichia coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The polynucleotide sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence encoded by a polynucleotide of the present invention. As used herein, the "functional portion" of a polypeptide is that portion which contains the active site essential for affecting the function of the polypeptide, for example, the portion of the molecule that is capable of binding one or more reactants. The active site may be made up

of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity.

Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using, for example, the representative assays provided below.

Portions and other variants of the inventive polypeptides may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2154, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed, site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82:488-492, 1985). Sections of polynucleotide sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

In general, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure. In certain embodiments, described in detail below, the isolated polypeptides are incorporated into pharmaceutical compositions or vaccines.

The present invention also contemplates methods for modulating the polynucleotide and/or polypeptide content and composition of an organism, such methods involving stably incorporating into the genome of the organism a construct containing DNA of the present invention. In one embodiment, the target  
5 organism is a mammal, preferably a human, for example for human gene therapy. In a related aspect, a method for producing an organism having an altered genotype or phenotype is provided, the method comprising transforming a cell with a DNA construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and  
10 mature organism growth.

The isolated polynucleotides of the present invention have utility in genome mapping, in physical mapping, and in positional cloning of genes. Additionally, the polynucleotide sequences identified as SEQ ID NOS: 1-35 and their variants may be used to design oligonucleotide probes and primers.  
15 Oligonucleotide probes and primers have sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. Oligonucleotide probes designed using the polynucleotides of the present invention may be used to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA  
20 sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the polynucleotides of the present invention may also be used in connection with various microarray  
25 technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

The polynucleotides of the present invention may also be used to tag or identify an organism or reproductive material therefrom. Such tagging may be accomplished, for example, by stably introducing a non-disruptive non-functional  
30 heterologous polynucleotide identifier into an organism, the polynucleotide comprising one of the polynucleotides of the present invention.

Detailed Description

Polynucleotides were isolated by high throughput sequencing of cDNA libraries prepared from mouse airway-induced eosinophilia, rat dermal papilla and mouse stromal cells as described below, in Example 1. Isolated polynucleotides of the present invention include the polynucleotides identified as SEQ ID NOS: 1-35; isolated polynucleotides comprising a polynucleotide sequence selected from the group consisting of SEQ ID NOS: 1-35; isolated polynucleotides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polynucleotides identified as SEQ ID NOS: 1-35; polynucleotides complementary to any of the above polynucleotides; anti-sense sequences corresponding to any of the above polynucleotides; and variants of any of the above polynucleotides, as that term is described in this specification. The present invention also provides isolated polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 36-65; polypeptide variants of those sequences; and polypeptides comprising the isolated polypeptide sequences and variants of those sequences.

The correspondence of isolated polynucleotides encoding isolated polypeptides of the present invention, and the functionality of the polypeptides, are shown, below, in Table 1.

Table 1

SEQ ID NO Poly-nucleotides	SEQ ID NO Poly-peptides	Activity Category	Functionality
1	36	Secretory molecule	Hypothetical 131.1 kDa protein
2	37	Secretory molecule/cytokine/cell signaling	ZCYTO7 belongs to a family of IL-17-related cytokines differing in patterns of expression and proinflammatory responses that may be transduced through a cognate set of cell surface receptors. IL-17 is a T cell-derived cytokine that may play an important role in the initiation or maintenance of the proinflammatory response. Whereas expression of IL-17 is restricted to activated T cells, the IL-17 receptor is found to be

			widely expressed, a finding consistent with the pleiotropic activities of IL-17.
3	38	Secretory molecule	Novel
4	39	Receptor/cytokine/ cell signaling	Tumor endothelial marker 1 precursor
5	40	Secretory molecule	ERO1-L (ERO1-like protein) is involved in oxidative endoplasmic reticulum (ER) protein folding in mammalian cells. Oxidizing conditions must be maintained in the ER to allow the formation of disulfide bonds in secretory proteins. A family of conserved genes, termed ERO for ER oxidoreductins, plays a key role in this process. ERO1-L is a type II integral membrane protein.
6	41	Secretory molecule	Novel
7	42	Receptor/transcription factor	EMR2 is an EGF-like module that is part of the epidermal growth factor (EGF)-TM7 proteins, which also include EMR1, (EGF-like molecule containing mucin-like hormone receptor 1) F4/80, and CD97. These proteins constitute a recently defined class B GPCR subfamily and are predominantly expressed on leukocytes. These molecules possess N-terminal EGF-like domains coupled to a seven-span transmembrane (7TM) moiety via a mucin-like spacer domain. EMR2 contains a total of five tandem EGF-like domains and expresses similar protein isoforms consisting of various numbers of EGF-like domains as a result of alternative RNA splicing. EMR2 share many characteristics with CD97, including highly homologous EGF-like domains and identical gene organization, indicating that both genes are the products of a recent gene duplication event. Both EMR2 and CD97 are highly expressed in immune tissues; however, unlike

			CD97, which is ubiquitously expressed in most cell types, EMR2 expression is restricted to monocytes, macrophages
8	43	Secretory molecule/ cell structure/motility, extracellular matrix	Bone/cartilage proteoglycan I (BGN) is also known as biglycan or PG-S1. BGN is found in the extracellular matrices of several connective tissues, especially in articular cartilages. The two glycosaminoglycan chains attached to BGN can be either chondroitin sulfate or dermatan sulfate. BGN belongs to the small interstitial proteoglycans family. BGN is a small leucine-rich proteoglycan and is a nonfibrillar extracellular matrix component with functions that include the positive regulation of bone formation. It is synthesized as a precursor with an NH(2)-terminal propeptide that is cleaved to yield the mature form found in vertebrate tissues. Bone morphogenetic protein-1 (BMP-1) cleaves proBGN at a single site, removing the propeptide and producing BGN. Soluble BGN purified from rat thymic myoid cells had hemopoietic activity capable of inducing preferential growth and differentiation of monocytic lineage cells from various hemopoietic sources, including brain microglial cells. The haemopoietic BGN plays an important role in generating brain-specific circumstances for development of microglial/monocytic cells
9	44	Secretory molecule	Tubulointerstitial nephritis antigen (TIN-ag) is a basement membrane glycoprotein reactive with autoantibodies in some forms of immunologically mediated human tubulointerstitial nephritis. TIN1 and TIN2 are alternatively spliced products of the TIN-Ag gene. The

			open reading frames of TIN1 and TIN2 indicates the presence of a signal peptide and putative pre-propeptide and both forms contain putative calcium-binding sites. TIN1 additionally contains a characteristic laminin-like epidermal growth factor (EGF) motif and significant homology within the carboxy terminus with the cysteine proteinase family of enzymes. The EGF motif bears important similarities in the positions of cysteines with two motifs in the propeptide of von Willebrand factor. The EGF motif and part of the region that is homologous with the cysteine proteinase family are removed from the TIN2 cDNA. The rest of the TIN1 and TIN2 sequences are identical. TIN-ag is expressed mainly in the kidney and in the intestinal epithelium.
10		Receptor-like molecule	Novel
11	45	Secretory molecule/ gene/protein expression, RNA synthesis, transcription factors	Toso is a cell surface, specific regulator of Fas-induced apoptosis in T cells. Fas is a surface receptor that can transmit signals for apoptosis. Toso is expressed in lymphoid cells and expression is enhanced after cell-specific activation processes in T cells. Toso appeared limited to inhibition of apoptosis mediated by members of the TNF receptor family and was capable of inhibiting T cell self-killing induced by TCR activation processes that up-regulate Fas ligand. Toso inhibits caspase-8 processing, the most upstream caspase activity in Fas-mediated signaling, potentially through activation of cFLIP. Toso therefore serves as a novel regulator of Fas-mediated apoptosis and may act as a regulator of cell fate in T cells and



			other hematopoietic lineages.
12	46	Secretory molecule/ gene/protein expression, RNA synthesis, transcription factors	<p>Surface glycoprotein CD59 is a phosphatidyl-inositol-glycan-anchored glycoprotein involved in T-cell activation and restriction of complement-mediated lysis. It is also known as protectin, and is ubiquitously expressed on benign and malignant cells. CD59 inhibits complement (C)-mediated lysis of target cells by preventing the formation of the membrane attack complex, in the terminal step of C-activation. Recent experimental evidence demonstrates that CD59 is the main restriction factor of C-mediated lysis of malignant cells of different histotypes. Additionally, a soluble form of CD59, that retains its anchoring ability and functional properties, has been identified in body fluids and in culture supernatants of different malignant cells. CD59 may protect neoplastic cells from C-mediated lysis, contributing to their escape from innate C-control and to tumor progression. The expression of CD59 by neoplastic cells may contribute to impair the therapeutic efficacy of C-activating monoclonal antibodies (mAb) directed to tumor-associated antigens. CD59 can be utilized to improve the therapeutic efficacy of clinical approaches of humoral immunotherapy with C-activating mAb in human malignancies.</p>
13	47	Secretory molecules/cell or organism defense, homeostasis, detoxification	<p>Cytochrome B561 (cyb561) is a secretory vesicle-specific electron transport protein unique to neuroendocrine secretory vesicles. It binds two heme groups non-covalently and is an integral membrane protein. It acts as an electron channel and mediates</p>

			equilibration of ascorbate-semidehydroascorbate inside the secretory vesicle with the ascorbate redox pair in the cytoplasm. The role for this function is to regenerate ascorbate inside the secretory vesicle for use by monooxygenases. The secretory vesicles contain catecholamines and amidated peptides. Cyb561 belongs to the eukaryotic b561 family.
14	48	Secretory molecule	Novel
15	49	Receptor-like molecule/ gene or protein expression, RNA synthesis, transcription factor	High affinity immunoglobulin epsilon receptor beta-subunit (FCER1) is also known as IgE Fc receptor, beta-subunit, FCER1b or FCE1b. FCER1 binds to the Fc region of immunoglobulins epsilon and is a high affinity receptor. FCER1 plays a role in initiating the allergic response where binding of allergen to receptor-bound IgE leads to cell activation and the release of mediators, such as histamine. FCER1 is responsible for the manifestations of allergy and induces the secretion of important lymphokines. It functions as a tetramer consisting of an alpha chain, a beta chain, and two disulfide-linked gamma chains and is an integral membrane protein. Variants of the FCER1B gene have been identified, which are associated with an increased risk of developing atopy and bronchial asthma. Atopic dermatitis is a common skin disease frequently associated with allergic disorders such as allergic rhinitis and asthma.
16	50	Receptor-like molecule	Hypothetical 10.3 kDa protein
17	51	Secretory molecule/antigen processing	Lysosomal thiol reductase IP30 catalyzes disulfide bond reduction both <i>in vitro</i> and <i>in vivo</i> and is optimally active at acidic pH. IP30

			is important in disulfide bond reduction of proteins delivered to MHC class II-containing compartments and consequently in antigen processing. IP30 can be mediated by multiple lysosomal proteases. Proteins internalized into the endocytic pathway are usually degraded. Efficient proteolysis requires denaturation, induced by acidic conditions within lysosomes, and reduction of inter- and intrachain disulfide bonds. The active site, determined by mutagenesis, consists of a pair of cysteine residues separated by two amino acids, similar to other enzymes of the thioredoxin family.
18		Receptor-like molecule	RNA binding protein.
19	52	Secretory molecule/cellular	Notch4-like protein (ZNEU1) is part of the NOTCH4 family that encodes receptors responsible for cell fate decisions during development. These Notch receptors and their ligands, Delta and Jagged, have been implicated in several diseases. When truncated, constitutively active mutant forms of the Notch receptor appear to be involved in T-cell leukemia, mammary carcinomas and a tumorous germline phenotype. Notch4 genes are expressed specifically in endothelial cells.
20	53	Secretory molecule	Novel
21	54	Secretory molecule/transporter	Serotransferrin (siderophilin) (Tf) or beta-1-metal binding globulin is part of the transferrin family. Transferrins are iron binding transport proteins which can bind two atoms of ferric iron in association with the binding of an anion, usually bicarbonate. Tf is responsible for the transport of iron from sites of absorption and heme degradation to those of storage and

			utilization. Serum transferrin also has a further role in stimulating cell proliferation. Tf gene expression is modulated by vitamin A, testosterone, and peptide hormones.
22	55	Secretory molecule/ gene or protein expression, RNA synthesis, transcription factor	Insulin-like growth factor binding protein 5 protease (IGFBP-5) modulates the effects of insulin growth factors (IGFs) on cells. IGFBP-5 is synthesized by smooth muscle cells and binds to the extracellular matrix. It is also secreted into conditioned medium of cultured cells and is cleaved into fragments by a concomitantly produced protease. These fragments have reduced affinity for the IGFs. IGFBP-5 protease belongs to a family of serine-metallo proteases.
23	56	Secretory molecule/cellular development	Major epididymis-specific protein E4 is also known as epididymal protein BE-20. It belongs to WAP-type 'four-disulfide core' family and plays a role in the maturation of spermatozoa during its movement through the epididymis and the capacity of sperm to fertilize ova. Expression of E4 was located to the epithelial cells of the cauda epididymis and proximal segment of the ductus deferens by in situ hybridization. No expression was found in sections of the corpus and caput epididymis, testis, and liver.
24		Secretory molecule/cell signaling	TNFR-related death receptor-6 DR6 contains an extracellular region containing varying numbers of cysteine-rich domains and an intracellular region that contains the death domain. Death receptors are activated in a ligand-dependent or independent manner and transduce apoptotic signals via their respective intracellular death domains.
25	57	Receptor-like molecule	Novel

26	58	Secretory molecule/regulation	Channel inducing factor precursor (CHIF) or corticosteroid-induced protein induces a potassium channel when expressed in <i>Xenopus</i> oocytes and activates endogenous oocyte transport proteins. It is a type I membrane protein selectively present in the distal parts of the nephron (medullary and papillary collecting ducts and end portions of cortical collecting tubule) and in the epithelial cells of the distal colon. No expression is found in renal proximal tubule, loop of Henle and distal tubule, proximal colon, small intestine, lung, choroid plexus, salivary glands, or brain. CHIF belongs to the ATP1G1 /PLM / Mat-8 family and exhibits significant homologies with proteins that are putatively regulatory (phospholemman, gamma-subunit of Na(+)-K(+)-ATPase, Mat-8).
27	59	Secretory molecule	Hepatocellular carcinoma-associated antigen 112.
28	60	Receptor-like molecule/homeostasis	Lymphatic endothelium-specific hyaluronan receptor LYVE-1 is a major receptor for hyaluronan (HA) on the lymph vessel wall molecule that binds both soluble and immobilized HA. LYVE-1 plays a role in the control of the HA pathway. The extracellular matrix glycosaminoglycan hyaluronan (HA) is an abundant component of skin and mesenchymal tissues where it facilitates cell migration during wound healing, inflammation, and embryonic morphogenesis. Both during normal tissue homeostasis and particularly after tissue injury, HA is mobilized from these sites through lymphatic vessels to the lymph nodes where it is degraded before entering the circulation for rapid uptake by the liver. LYVE-1 is similar to the

			CD44 HA receptor, but in contrast to CD44, LYVE-1 colocalizes with HA on the luminal face of the lymph vessel wall and is completely absent from blood vessels.
29	61	Receptor-like molecule/cell signaling	G protein-coupled receptor GPR35 is an integral membrane protein that belongs to family 1 of G-protein coupled receptors (GPCR). The GPCR family shares a structural motif of seven transmembrane segments with large numbers of conserved residues in those regions.
30	62	Receptor-like molecule	Tumor-associated glycoprotein E4 is also known as Taa1 or Tage4 and belongs to the immunoglobulin superfamily. This family contains cell adhesion molecules which have wide-ranging functions and mediate a variety of homotypic and heterotypic cellular interactions playing a general role in cell surface recognition. The Tage4 gene product is closely related to the hepatocellular carcinoma antigen TuAg.1. Tage4 is a glycoprotein expressed at the surface of colon carcinoma cell lines, but at a very low level in normal adult colon and lung tissue and not in normal tissues tested.
31	63	Secretory molecule	Hypothetical 28.6 kDa protein is also known as plunc, for palate, lung, and nasal epithelium clone. Expression of plunc is associated with the palate, nasal septum, and nasal conchae. It is also expressed strongly in the trachea and bronchi of the adult lung. No significant homologies with known genes were observed at the nucleotide level and limited amino acid homology with two salivary gland-specific proteins was noted. The amino acid sequence revealed consensus sequences for N-glycosylation, protein kinase C and

			casein kinase phosphorylation, as well as a leucine zipper. In addition, an unique amino acid sequence repeat sequence is located near the amino-terminal portion of the protein.
32	64	Secretory molecule	<p>Claudin-18 (Cldn18) is a component of tight junction (TJ) strands and belongs to the claudin family. Claudins are integral membrane protein component of tight junctions, a structure controlling cell-to-cell adhesion and, consequently, regulating paracellular and transcellular transport of solutes across epithelia and endothelia. The claudin family also includes occludin and 17 other distinct claudins. Claudin family members are tetra-span transmembrane proteins that are localized in cell-specific TJs. In multicellular organisms, various compositionally distinct fluid compartments are established by epithelial and endothelial cellular sheets. For these cells to function as barriers, TJs are considered to create a primary barrier for the diffusion of solutes through the paracellular pathway. Claudins are therefore responsible for TJ-specific obliteration of the intercellular space.</p>
33		Secretory molecule	<p>Glutamine repeat protein 1 (GRP-1) contains simple tandem repeats of the trinucleotide sequence CAG that encode homopolymeric stretches of glutamine. Although polyglutamine has been identified in diverse proteins, it is present predominantly in transcription factors. Greater than two-thirds of GRP-1 are only two amino acids, namely glutamine (50%) and histidine (18%). There are four polyglutamine motifs interspersed with histidine-rich regions. There is also a putative</p>

			nuclear localization signal flanked by sites for possible serine phosphorylation. GRP-1 mRNA was expressed constitutively in some macrophage cell lines and B and T cell lines. Interferon-gamma or lipopolysaccharide augmented GRP-1 mRNA expression in the mouse macrophage cell line ANA-1. Because polyglutamine motifs can cause protein oligomerization and can function as transcriptional activation domains, GRP-1 is a transcription factor associated with interferon-gamma- or lipopolysaccharide-induced activation of macrophages.
34		Secretory molecule	Alpha-1 collagen
35	65	Receptor-like molecule/Cell signaling	Gdnf family receptor alpha 4, transmembrane isoform (Gfra4) is a members of the Gdnf protein family that signal through receptors consisting of a GPI-linked GFRalpha subunit and the transmembrane tyrosine kinase Ret. Gfra4 is expressed in many tissues, including nervous system, in which intron retention leads to a putative intracellular or secreted GFRalpha4 protein. Efficient splicing occurs only in thyroid, parathyroid, and pituitary and less in adrenal glands. A splice form that leads to a GPI-linked GFRalpha4 receptor is expressed in juvenile thyroid and parathyroid glands. In newborn and mature thyroid as well as in parathyroid and pituitary glands major transcripts encode for a putative transmembrane isoform of GFRalpha4. GFRalpha4 expression may restrict the inherited cancer syndrome multiple endocrine neoplasia type 2, associated with mutations in RET, to these cells.



The word "polynucleotide(s)," as used herein, means a polymeric collection of nucleotides and includes DNA and corresponding RNA molecules and both single and double stranded molecules, including HnRNA and mRNA molecules, sense and anti-sense strands of DNA and RNA molecules, and comprehends cDNA, genomic DNA, and wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and "corresponds to" a DNA molecule in a generally one-to-one manner. An mRNA molecule "corresponds to" an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide of the present invention may be an entire gene, or any portion thereof. A gene is a DNA sequence which codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23): 363-375, 1995 and Kawasaki *et al.*, *Artific. Organs* 20 (8): 836-848, 1996.

Identification of genomic DNA and heterologous species DNA can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a cDNA sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and/or protein sequences can be used to amplify and identify genomic and cDNA sequences. Synthetic DNA corresponding to the identified sequences and variants may be produced by conventional synthesis methods. All of the polynucleotides described herein are isolated and purified, as those terms are commonly used in the art.

As used herein, the term "oligonucleotide" refers to a relatively short segment of a polynucleotide sequence, generally comprising between 6 and 60 nucleotides, and comprehends both probes for use in hybridization assays and primers for use in the amplification of DNA by polymerase chain reaction.

As used herein, the term "x-mer," with reference to a specific value of "x," refers to a polynucleotide comprising at least a specified number ("x") of contiguous residues of any of the polynucleotides identified as SEQ ID NOS: 1-35. The value of  $x$  may be from about 20 to about 600, depending upon the specific sequence.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full-length proteins, wherein amino acid residues are linked by covalent peptide bonds. Polypeptides of the present invention may be naturally purified products, or may be produced partially or wholly using recombinant techniques. Such polypeptides may be glycosylated with mammalian or other eukaryotic carbohydrates or may be non-glycosylated.

According to one embodiment, "variants" of the polynucleotides of the present invention, including the polynucleotides set forth as SEQ ID NOS: 1-35, as that term is used herein, comprehends polynucleotides producing an "E" value of 0.01 or less, as described below, or having at least a specified percentage identity to a polynucleotide of the present invention, as described below. Polynucleotide variants of the present invention may be naturally occurring allelic variants, or non-naturally occurring variants.

Polynucleotide and polypeptide sequences may be aligned, and percentages of identical residues in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. Polynucleotides may also be analyzed using the BLASTX algorithm, which compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. The percentage identity of polypeptide sequences may be examined using the BLASTP algorithm. The BLASTN, BLASTP and BLASTX algorithms are available on the NCBI anonymous FTP server (<ftp://ncbi.nlm.nih.gov>) under /blast/executables/ and are available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894,

USA. The BLASTN algorithm Version 2.0.11 [Jan-20-2000], set to the parameters described below, is preferred for use in the determination of polynucleotide variants according to the present invention. The BLASTP algorithm, set to the parameters described below, is preferred for use in the determination of polypeptide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described at NCBI's website at URL <http://www.ncbi.nlm.nih.gov/BLAST/newblast.html> and in the publication of Altschul, *et al.*, *Nucleic Acids Res.* 25: 3389-3402, 1997.

10 The FASTA and FASTX algorithms are available on the Internet at the ftp site <ftp://ftp.virginia.edu/pub/>, and from the University of Virginia by contacting David Hudson, Vice Provost for Research, University of Virginia, P.O. Box 9025, Charlottesville, VA 22906-9025, USA. The FASTA algorithm, set to the default parameters described in the documentation and distributed with the algorithm, 15 may be used in the determination of polynucleotide variants. The readme files for FASTA and FASTX Version 1.0x that are distributed with the algorithms describe the use of the algorithms and describe the default parameters. The use of the FASTA and FASTX algorithms is described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and Pearson, *Methods in Enzymol.* 20 183:63-98, 1990. The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the E values and percentage identity: Unix running command with default parameter values thus: `blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq -o results`; the Parameters are : -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v 25 Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File 30 Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN or FASTA or a similar algorithm align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally  
5 represent an overlap over only a fraction of the sequence length of the queried sequence.

The BLASTN and FASTA algorithms produce "Expect" values for alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a  
10 database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database, such as the preferred EMBL database, indicates true similarity. For example, an E value of 0.1 assigned to a hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a  
15 similar score simply by chance. The aligned and matched portions of the sequences, then, have a probability of 90% of being the same by this criterion. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN or FASTA algorithm.

20 According to one embodiment, "variant" polynucleotides, with reference to each of the polynucleotides of the present invention, preferably comprise sequences having the same number or fewer nucleic acids than each of the polynucleotides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide of the present invention. That is, a variant  
25 polynucleotide is any sequence that has at least a 99% probability of being the same as the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or FASTA algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of  
30 the present invention that has at least a 99% probability of being the same as the

polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or FASTA algorithms set at the default parameters.

Alternatively, variant polynucleotides of the present invention may comprise a sequence exhibiting at least about 40%, more preferably at least about 5 60%, more preferably yet at least about 75%, and most preferably at least about 90% similarity to a polynucleotide of the present invention, determined as described below. The percentage similarity is determined by aligning sequences using one of the BLASTN or FASTA algorithms, set at default parameters, and identifying the number of identical nucleic acids over the best aligned portion; 10 dividing the number of identical nucleic acids by the total number of nucleic acids of the polynucleotide of the present invention; and then multiplying by 100 to determine the percentage similarity. For example, a polynucleotide of the present invention having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the 15 alignment produced by the BLASTN algorithm using the default parameters. The 23 nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage similarity of the polynucleotide of the present invention to the hit in the EMBL library is thus  $21/220$  times 100, or 9.5%. The polynucleotide sequence in the EMBL database is thus not a variant of a 20 polynucleotide of the present invention.

Alternatively, variant polynucleotides of the present invention hybridize to a polynucleotide of the present invention under stringent hybridization conditions. As used herein, "stringent conditions" mean prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two 25 washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses allelic variants of the disclosed sequences, together with DNA sequences that differ from the disclosed sequences but which, due to the degeneracy of the genetic code, encode a polypeptide which 30 is the same as that encoded by a DNA sequence disclosed herein. Thus, polynucleotides comprising sequences that differ from the polynucleotide

sequences recited in SEQ ID NOS: 1-35, or complements, reverse sequences, or reverse complements of those sequences as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NOS: 1-35, or complements, reverse complements, or reverse sequences as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention.

The polynucleotides of the present invention may be isolated from various DNA libraries, or may be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (e.g. Beckman Oligo 1000M DNA Synthesizer) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5-nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5-nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

SEQ ID NOS: 2, 3, 5, 7-9, 11, 12, 14, 15, 17, 19-21, 23, 26, 28 and 30-32 are full-length sequences. The remaining polynucleotides are referred to as "partial" sequences, in that they may not represent the full coding portion of a gene encoding a naturally occurring polypeptide. The partial polynucleotide sequences disclosed herein may be employed to obtain the corresponding full-length genes for various species and organisms by, for example, screening DNA expression libraries using hybridization probes based on the polynucleotides of the present invention, or using PCR amplification with primers based upon the

polynucleotides of the present invention. In this way one can, using methods well known in the art, extend a polynucleotide of the present invention upstream and downstream of the corresponding mRNA, as well as identify the corresponding genomic DNA, including the promoter and enhancer regions, of the complete gene. The present invention thus comprehends isolated polynucleotides comprising a sequence identified in SEQ ID NOS: 1-35, or a variant of one of the specified sequences, that encode a functional polypeptide, including full-length genes. Such extended polynucleotides may have a length of from about 50 to about 4,000 nucleic acids or base pairs, and preferably have a length of less than about 4,000 nucleic acids or base pairs, more preferably yet a length of less than about 3,000 nucleic acids or base pairs, more preferably yet a length of less than about 2,000 nucleic acids or base pairs. Under some circumstances, extended polynucleotides of the present invention may have a length of less than about 1,800 nucleic acids or base pairs, preferably less than about 1,600 nucleic acids or base pairs, more preferably less than about 1,400 nucleic acids or base pairs, more preferably yet less than about 1,200 nucleic acids or base pairs, and most preferably less than about 1,000 nucleic acids or base pairs.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues ( $x$ -mers) of any of the polynucleotides identified as SEQ ID NOS: 1-35 or their variants. According to preferred embodiments, the value of  $x$  is preferably at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide identified as SEQ ID NOS: 1-35 or a variant of one of the polynucleotides identified as SEQ ID NOS: 1-35.

Polynucleotide probes and primers complementary to and/or corresponding to SEQ ID NOS: 1-35, and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest. An

oligonucleotide probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NOS: 1-35 or a variant, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-35 or a variant of one of the specified sequences.

Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared using, for example, the BLAST algorithm as described above, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a second DNA strand under stringent hybridization conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C and most preferably greater than about 37°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as probe composition, presence of organic solvents and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. The DNA from plants or samples or products containing plant material can be either genomic DNA or DNA derived by preparing cDNA from the RNA present in the sample.

In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the case of DNA-RNA hybridization, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the case of RNA-RNA hybridization, RNA probes could be used. In addition, artificial analogs of DNA hybridizing specifically to target sequences could also be employed.



In specific embodiments, the oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and  
5 primers of the present invention may be from about 8 to 100 base pairs in length or, preferably from about 10 to 50 base pairs in length or, more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops  
10 and other factors, which are well known in the art. Tools and software suitable for designing probes, and especially suitable for designing PCR primers, are available on the Internet, for example, URL <http://www.horizonpress.com/pcr/>. Preferred techniques for designing PCR primers are also disclosed in Dieffenbach and Dykster, *PCR primer: a laboratory manual*. Cold Spring Harbor Laboratory  
15 Press, Cold Spring Harbor, NY, 1995.

A plurality of oligonucleotide probes or primers corresponding to a polynucleotide of the present invention may be provided in a kit form. Such kits generally comprise multiple DNA or oligonucleotide probes, each probe being specific for a polynucleotide sequence. Kits of the present invention may  
20 comprise one or more probes or primers corresponding to a polynucleotide of the present invention, including a polynucleotide sequence identified in SEQ ID NOS: 1-35.

In one embodiment useful for high-throughput assays, the oligonucleotide probe kits of the present invention comprise multiple probes in an array format,  
25 wherein each probe is immobilized in a predefined, spatially addressable location on the surface of a solid substrate. Array formats which may be usefully employed in the present invention are disclosed, for example, in U.S. Patents No. 5,412,087, 5,545,531, and PCT Publication No. WO 95/00530, the disclosures of which are hereby incorporated by reference.

30 Oligonucleotide probes for use in the present invention may be constructed synthetically prior to immobilization on an array, using techniques well known in

the art (see, for example, *Oligonucleotide Synthesis: A Practical Approach*, Gait, ed., IRL Press, Oxford, 1984). Automated equipment for the synthesis of oligonucleotides is available commercially from such companies as Perkin Elmer/Applied Biosystems Division (Foster City, CA) and may be operated  
5 according to the manufacturer's instructions. Alternatively, the probes may be constructed directly on the surface of the array using techniques taught, for example, in PCT Publication No. WO 95/00530.

The solid substrate and the surface thereof preferably form a rigid support and are generally formed from the same material. Examples of materials from  
10 which the solid substrate may be constructed include polymers, plastics, resins, membranes, polysaccharides, silica or silica-based materials, carbon, metals and inorganic glasses. Synthetically prepared probes may be immobilized on the surface of the solid substrate using techniques well known in the art, such as those disclosed in U.S. Patent No. 5,412,087.

15 In one such technique, compounds having protected functional groups, such as thiols protected with photochemically removable protecting groups, are attached to the surface of the substrate. Selected regions of the surface are then irradiated with a light source, preferably a laser, to provide reactive thiol groups. This irradiation step is generally performed using a mask having apertures at  
20 predefined locations using photolithographic techniques well known in the art of semiconductors. The reactive thiol groups are then incubated with the oligonucleotide probe to be immobilized. The precise conditions for incubation, such as temperature, time and pH, depend on the specific probe and can be easily determined by one of skill in the art. The surface of the substrate is washed free of  
25 unbound probe and the irradiation step is repeated using a second mask having a different pattern of apertures. The surface is subsequently incubated with a second, different, probe. Each oligonucleotide probe is typically immobilized in a discrete area of less than about 1 mm<sup>2</sup>. Preferably each discrete area is less than about 10,000 mm<sup>2</sup>, more preferably less than about 100 mm<sup>2</sup>. In this manner, a  
30 multitude of oligonucleotide probes may be immobilized at predefined locations on the array.

The resulting array may be employed to screen for differences in organisms or samples or products containing genetic material as follows. Genomic or cDNA libraries are prepared using techniques well known in the art. The resulting target DNA is then labeled with a suitable marker, such as a radiolabel, chromophore, fluorophore or chemiluminescent agent, using protocols well known for those skilled in the art. A solution of the labeled target DNA is contacted with the surface of the array and incubated for a suitable period of time.

The surface of the array is then washed free of unbound target DNA and the probes to which the target DNA hybridized are determined by identifying those regions of the array to which the markers are attached. When the marker is a radiolabel, such as  $^{32}\text{P}$ , autoradiography is employed as the detection method. In one embodiment, the marker is a fluorophore, such as fluorescein, and the location of bound target DNA is determined by means of fluorescence spectroscopy. Automated equipment for use in fluorescence scanning of oligonucleotide probe arrays is available from Affymetrix, Inc. (Santa Clara, CA) and may be operated according to the manufacturer's instructions. Such equipment may be employed to determine the intensity of fluorescence at each predefined location on the array, thereby providing a measure of the amount of target DNA bound at each location. Such an assay would be able to indicate not only the absence and presence of the marker probe in the target, but also the quantitative amount as well.

In this manner, oligonucleotide probe kits of the present invention may be employed to examine the presence/absence (or relative amounts in case of mixtures) of polynucleotides in different samples or products containing different materials rapidly and in a cost-effective manner.

Another aspect of the present invention involves collections of a plurality of polynucleotides of the present invention. A collection of a plurality of the polynucleotides of the present invention, particularly the polynucleotides identified as SEQ ID NOS: 1-35, may be recorded and/or stored on a storage medium and subsequently accessed for purposes of analysis, comparison, etc. One utility for such sets of sequences is the analysis of the set, either alone or together with other sequences sets, for single nucleotide polymorphisms (SNPs)

between sequences from different tissues and/or individuals for genetic studies, mapping and fingerprinting purposes. Suitable storage media include magnetic media such as magnetic diskettes, magnetic tapes, CD-ROM storage media, optical storage media, and the like. Suitable storage media and methods for recording and storing information, as well as accessing information such as polynucleotide sequences recorded on such media, are well known in the art. The polynucleotide information stored on the storage medium is preferably computer-readable and may be used for analysis and comparison of the polynucleotide information.

10 Another aspect of the present invention thus involves storage medium on which are recorded a collection of the polynucleotides of the present invention, particularly a collection of the polynucleotides identified as SEQ ID NOS: 1-35. According to one embodiment, the storage medium includes a collection of at least 20, preferably at least 50, more preferably at least 100, and most preferably  
15 at least 200 of the polynucleotides of the present invention, preferably the polynucleotides identified as SEQ ID NOS: 1-35, or variants of those polynucleotides.

Another aspect of the present invention involves a combination of polynucleotides, the combination containing at least 5, preferably at least 10, more  
20 preferably at least 20, and most preferably at least 50 different polynucleotides of the present invention, including polynucleotides selected from SEQ ID NOS: 1-35, or variants of these polynucleotides.

In another aspect, the present invention provides DNA constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading  
25 frame coding for at least a functional portion of a polypeptide encoded by a polynucleotide of the present invention; and a gene termination sequence. The open reading frame may be orientated in either a sense or antisense direction. DNA constructs comprising a non-coding region of a gene coding for an enzyme encoded by the above DNA sequences or a nucleotide sequence complementary to  
30 a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and

termination sequences are functional in a host cell. More preferably, the gene promoter and termination sequences are common to those of the polynucleotide being introduced. Other promoter and termination sequences generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without  
5 enhancers, such as the Kozak sequence or Omega enhancer, and *Agrobacterium tumefaciens* nopal synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. The DNA construct may further include a marker for the identification of transformed cells.

10 Techniques for operatively linking the components of the DNA constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, *Molecular Cloning: a laboratory manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. The DNA constructs of the present invention  
15 may be linked to a vector having at least one replication system, for example, *Escherichia coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced and the correctness of the manipulation determined.

Transgenic cells comprising the DNA constructs of the present invention are provided, together with organisms comprising such transgenic cells.  
20 Techniques for stably incorporating DNA constructs into the genome of target organisms, such as mammals, are well known in the art and include electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target organism to be transformed. In  
25 one embodiment, naked DNA is injected or delivered orally. Once the cells are transformed, cells having the DNA construct incorporated in their genome are selected. Transgenic cells may then be cultured in an appropriate medium, using techniques well known in the art.

In yet a further aspect, the present invention provides methods for  
30 modifying the level (concentration) or activity of a polypeptide in a host organism, comprising stably incorporating into the genome of the organism a

DNA construct of the present invention. The DNA constructs of the present invention may be used to transform a variety of organisms, including mammals, for example to make experimental gene knock out or transgenic animals.

Further, the polynucleotides of the present invention have particular application for use as non-disruptive tags for marking organisms, including commercially valuable animals, fish, bacteria and yeasts. DNA constructs comprising polynucleotides of the present invention may be stably introduced into an organism as heterologous, non-functional, non-disruptive tags. It is then possible to identify the origin or source of the organism at a later date by determining the presence or absence of the tag(s) in a sample of material.

Detection of the tag(s) may be accomplished using a variety of conventional techniques, and will generally involve the use of nucleic acid probes. Sensitivity in assaying the presence of probe can be usefully increased by using branched oligonucleotides, as described by Horn *et al.*, *Nucleic Acids Res.* 25(23):4842-4849, 1997, enabling to detect as few as 50 DNA molecules in the sample.

In particular, the polynucleotides of the present invention encode polypeptides that have important roles in processes such as induction of growth, differentiation of tissue-specific cells, cell migration, cell proliferation, and cell-cell interaction. These polypeptides are important in the maintenance of tissue integrity, and thus are important in processes such as wound healing. Some of these polypeptides act as modulators of immune responses, such as immunologically active polypeptides for the benefit of offspring. In addition, many polypeptides are immunologically active, making them important therapeutic targets in a whole range of disease states. Antibodies to the polypeptides of the present invention and small molecule inhibitors related to the polypeptides of the present invention may also be used for modulating immune responses and for treatment of diseases according to the present invention.

SEQ ID NOS: 1; 2; 4; 5; 6; 8; 9; 11; 12; 14; 17; 19-24; 26; 27; 31-34 encode secreted polypeptides. SEQ ID NOS: 10; 15; 16; 18; 25; 28; 30; and 35 encode polypeptides acting as receptors. SEQ ID NOS: 2; 4; 24; 29 and 35

encode polypeptides with cell signaling activity, which may be either intracellular or extracellular. Kinase genes, for example, encode polypeptides that phosphorylate specific substrates during cell-to-cell signaling. While some kinases are involved in normal metabolism and nucleotide production, others are significant for altering the activity of many cellular processes through the phosphorylation of specific proteins. Polypeptides encoded by these genes are important in the transmission of intracellular signals resulting from the binding of extracellular ligands such as hormones, growth factors or cytokines to membrane-bound receptors. The utility of polynucleotides encoding kinases resides in the manipulation of their signaling activities and downstream effects for the diagnosis and treatment of mammalian diseases that may be a consequence of inappropriate expression of these kinase genes.

SEQ ID NOS: 2 and 4 encode polypeptides with cytokine activity. Cytokine or growth factor polynucleotides encode polypeptides involved in intercellular signaling and represent another important class of molecules. Polynucleotides encoding such genes have utility in the diagnosis and treatment of disease.

SEQ ID NOS: 7; 11; 12; 15 and 22 encode polypeptides with transcription factor activity. These polynucleotides encode polypeptides required for the control of synthesis of proteins in tissue specific manner and have utility for the modification of protein synthesis for the control of disease.

SEQ ID NOS: 8 encode polypeptides acting in the extracellular matrix.

SEQ ID NOS: 11; 12; 15 and 22 encode polypeptides with RNA synthesis activities.

SEQ ID NO: 12 encodes a polypeptide having CD antigen activity. Such polynucleotides have utility as modulators of the composition, expression level and class of CD antigen expressed, which influence immune responses to self-antigens, neo-antigens and infectious agents.

Further exemplary specific utilities, for exemplary polynucleotides of the present invention, are specified in the Table below.

SEQ ID NO:	UTILITY
2	Promoting immune response as part of a vaccine or anti-cancer treatment. Inhibitors of this molecule can be useful as anti-inflammatory treatment, e.g. for autoimmune diseases or allergies.
11; 19	Utility as a target for cancer treatment and as an immunoregulatory and anti-inflammatory molecule
12	Diagnostic for specific types of cancer and for development of an anti-cancer treatment.
15	As a target for antagonists in the treatment of diseases such as asthma and allergy.
22	Useful to inhibit or enhance the activity of the soluble molecule that binds this protein.
28	Useful to promote or block cell trafficking and therefore in the treatment as anti-inflammatory and/or vaccine adjuvant where it can promoter inflammation.
35	Useful for tissue and neural regeneration.

The following examples are offered by way of illustration and not by way of limitation.

5

### Example 1

#### ISOLATION OF CDNA SEQUENCES FROM MAMMALIAN EXPRESSION LIBRARIES

The cDNA sequences of the present invention were obtained by high-throughput sequencing of cDNA expression libraries constructed mouse airways-induced eosinophilia, rat dermal papilla and mouse stromal cells. The cDNA  
10 libraries were prepared as follows.

#### *cDNA Library from Dermal Papilla (DEPA)*

Dermal papilla cells from rat hair vibrissae (whiskers) were grown in  
15 culture and the total RNA extracted from these cells using established protocols. Total RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's



specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

5 *cDNA library from mouse airway-induced eosinophilia (MALA)*

Airway eosinophilia were induced in BALB/cByJ mice by administering 2 µg ovalbumin in 2 mg alum adjuvant intraperitoneally on day 0 and day 14, and subsequently 100 µg ovalbumin in 50 µl phosphate buffered saline (PBS) intranasally route on day 28. The accumulated eosinophils in the lungs were  
10 detected by washing the airways of the anesthetized mice with saline, collecting the washings (broncheolar lavage or BAL), and counting the numbers of eosinophils. The mice were sacrificed and total RNA was isolated from whole lung tissue using TRIzol Reagent (BRL Life Technologies). mRNA was isolated by using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA),  
15 according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit (Stratagene).

*cDNA Expression Library from Peripheral Lymph Node Stromal Cells (MLSA)*

20 The peripheral axillary and brachial lymph nodes of BALB/cByJ mice with the flaky skin (*fsn*) mutation (Jackson Laboratories, Bar Harbour, MN) were dissected out. Single cell suspensions were obtained from the lymph nodes and cultured in tissue culture flasks at  $10^7$  cells /ml in 20% fetal calf serum and Dulbecco's Minimum Essential Medium. After 2 days the non-adherent cells were  
25 removed. The adherent cells were cultured for a further 2 days and then treated with 0.25 g/100ml Trypsin (ICN, Aurora, OH) and re-cultured. After a further 4 days, non-adherent cells were discarded and adherent cells removed by trypsinization. Remaining adherent cells were physically removed by scraping with a rubber policeman. All adherent stromal cells were pooled.

*cDNA Expression Library from Flaky skin lymph node stromal cells in pBK-CMV (MLSA)*

Stromal cells from Flaky skin mice lymph nodes were grown in culture and the total RNA extracted from these cells using established protocols. Total  
5 RNA, isolated using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD), was used to obtain mRNA using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. A cDNA expression library was then prepared from the mRNA by reverse transcriptase synthesis using a Lambda ZAP cDNA library synthesis kit  
10 (Stratagene).

cDNA sequences were obtained by high-throughput sequencing of the cDNA libraries described above using a Prism 377 sequencer (Perkin Elmer/Applied Biosystems Division, Foster City CA), and are provided in SEQ ID NO: 1-35, with corresponding polypeptide sequences in SEQ ID NOS: 36-65.

15

## EXAMPLE 2

### Analysis of cDNA sequences using BLAST algorithms

#### BLASTN Polynucleotide analysis

20 The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. Comparisons of DNA sequences provided in SEQ ID NOS: 1-35, to sequences in the EMBL DNA database (using BLASTN) were made as of November, 2000, using Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall -p  
25 blastn -d embldb -e 10 -G0 -E0 -r 1 -v 30 -b 30 -i queryseq -o.

The sequences of SEQ ID NOS: 1, 3, 4, 6-11, 13, 18, 21, 22, 24, 25, 28-30, 33 and 34 were determined to have less than 50% identity, determined as described above, to sequences in the EMBL database using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NOS: 2, 12,  
30 14-16, 20 and 35 were determined to have less than 75% identity, determined as described above, to sequences in the EMBL database using the computer

algorithm BLASTN, as described above. The sequences of SEQ ID NOS: 17, 19, 23 and 27 were determined to have less than 90% identity, determined as described above, to sequences in the EMBL database using the computer algorithm BLASTN, as described above. Finally, the sequences of SEQ ID NOS: 5, 26 and 32 were determined to have less than 98% identity, determined as described above, to sequences in the EMBL database using the computer algorithm BLASTN, as described above.

#### BLASTP Polypeptide analysis

10 The sequences of SEQ ID NOS: 37, 41, 42, 44, 46-50, 55, 56 and 59 were determined to have less than 50% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 36, 38, 43, 45 and 60 were determined to have less than 75% identity, determined as described above, to  
15 sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NOS: 39, 54 and 58 were determined to have less than 90% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. Finally, the sequences of SEQ ID NOS: 53, 57, 62 and 65 were determined to  
20 have less than 98% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTP, as described above.

#### BLASTX Polynucleotide Analysis

25 The sequences of SEQ ID NOS: 2-4, 6-16, 18, 22-24, 26-30 and 33-35 were determined to have less than 50% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NOS: 1, 19, 20, 25 and 32 were determined to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as  
30 described above. Finally, the sequences of SEQ ID NOS: 5, 17, 21 and 31 were determined to have less than 90% identity, determined as described above, to

sequences in the SwissProt database using the computer algorithm BLASTX, as described above.

5

### Example 2

#### ISOLATION AND CHARACTERIZATION OF THE HUMAN HOMOLOG OF MUKS1

This example demonstrates that an isolated cDNA may be used to isolate its homologue from a different species, the corresponding polypeptide may be expressed and the function of the polypeptide can be determined, starting the whole process from an isolated cDNA obtained as described above.

#### *Analysis of RNA transcripts by Northern Blotting*

Northern analysis to determine the size and distribution of mRNA for the clone muKS1 (SEQ ID NO: 66; isolated from a mouse keratinocyte stem cell cDNA library using high-throughput sequencing as described above) was performed by probing murine tissue mRNA blots with a probe consisting of nucleotides 268-499 of muKS1, radioactively labeled with [ $\alpha^{32}\text{P}$ ]-dCTP. Prehybridization, hybridization, washing and probe labeling were performed as described in Sambrook *et al.*, *Ibid.* mRNA for muKS1 was 1.6 kb in size and was observed to be most abundant in brain, lung, muscle and heart. Expression could also be detected in lower intestine, skin and kidney. No detectable signal was found in testis, spleen, liver, thymus and stomach.

#### 25 *Human homologue of muKS1*

MuKS1 (SEQ ID NO: 66) was used to search the EMBL database (Release 50 plus updates to June, 1998) to identify human EST homologues. The top three homologues were to the following ESTs: accession numbers AA643952, HS1301003 and AA865643. These showed 92.63% identity over 285 nucleotides, 93.64% over 283 nucleotides and 94.035% over 285 nucleotides, respectively. Frame shifts were identified in AA643952 and HS1301003 when

translated. Combination of all three ESTs identified the human homologue huKS1 (SEQ ID NO: 67) and translated polypeptide SEQ ID NO: 67. Alignment of muKS1 and huKS1 polypeptides indicated 95% identity over 96 amino acids.

#### 5 *Bacterial expression and purification of muKS1 and huKS1*

Polynucleotides 269-502 of muKS1 (SEQ ID NO: 69), encoding amino acids 23-99 of polypeptide muKS1 (SEQ ID NO: 70), and polynucleotides 55-288 of huKS1 (SEQ ID NO: 71), encoding amino acids 19-95 of polypeptide huKS1 (SEQ ID NO: 72), were cloned into the bacterial expression vector pET-16b  
10 (Novagen, Madison, WI), which contains a bacterial leader sequence and N-terminal 6xHistidine tag. These constructs were transformed into competent *E. coli* BL21(DE3) (Novagen) as described in Sambrook *et al.*, *Ibid*.

Starter cultures of recombinant *E. coli* BL21(DE3) (Novagen) transformed with bacterial expression vector pET16b containing SEQ ID NO: 69 (muKS1a) and SEQ ID NO: 71 (huKS1a) were grown in NZY broth containing 100 µg/ml  
15 ampicillin (Gibco-BRL Life Technologies) at 37°C. Cultures were spun down and used to inoculate 800 ml of NZY broth and 100 µg/ml ampicillin. Cultures were grown until the OD<sub>595</sub> of the cells was between 0.4 and 0.8. Bacterial expression was induced for 3 hours with 1 mM IPTG. Bacterial expression produced an  
20 induced band of approximately 15 kDa for muKS1a and huKS1a.

MuKS1a and huKS1a were expressed in insoluble inclusion bodies. In order to purify the polypeptides, bacterial cell pellets were re-suspended in lysis buffer (20 mM Tris-HCl pH 8.0, 10 mM β-Mercaptoethanol, 1 mM PMSF). To the lysed cells, 1% NP-40 was added and the mix incubated on ice for 10 minutes.  
25 Lysates were further disrupted by sonication on ice at 95 W for 4 x 15 seconds and then centrifuged for 10 minutes at 18,000 rpm to pellet the inclusion bodies.

The pellet containing the inclusion bodies was re-suspended in lysis buffer containing 0.5% w/v CHAPS and sonicated for 5-10 seconds. This mix was stored on ice for 1 hour, centrifuged at 14,000 rpm for 15 minutes at 4°C and the  
30 supernatant discarded. The pellet was once more re-suspended in lysis buffer

containing 0.5% w/v CHAPS, sonicated, centrifuged and the supernatant removed as before. The pellet was re-suspended in solubilizing buffer (6 M guanidine HCl, 0.5 M NaCl, 20 mM Tris-HCl pH 8.0), sonicated at 95 W for 4 x 15 sec and centrifuged for 10 minutes at 18,000 rpm and 4°C to remove debris. The supernatant was stored at 4°C. MuKS1a and huKS1a were purified by virtue of the N-terminal 6x histidine tag contained within the bacterial leader sequence, using a Nickel-Chelating sepharose column (Amersham Pharmacia, Uppsala, Sweden) and following the manufacturer's protocol. Proteins were purified twice over the column to reduce endotoxin contamination. In order to re-fold the proteins once purified, the protein solution was dialysed in a 4 M-2 M urea gradient in 20 mM Tris-HCl pH 7.5 containing 10% glycerol overnight at 4°C. The protein was then further dialysed 2x against 2 litres of 20 mM Tris-HCl pH 7.5 containing 10% glycerol.

*Injection of bacterially expressed muKS1a into nude mice*

Two nude mice were anaesthetised intraperitoneally with 75 µl of 1/10 dilution of Hypnorm (Janssen Pharmaceuticals, Buckinghamshire, England) in phosphate buffered saline. 20 µg of bacterially expressed muKS1a (SEQ ID NO: 70) was injected subcutaneously in the left hind foot, ear and left hand side of the back. The same volume of phosphate buffered saline was injected in the same sites but on the right hand side of the same animal. Mice were left for 18 hours and then examined for inflammation. Both mice showed a red swelling in the ear and foot sites injected with the bacterially expressed protein. No obvious inflammation could be identified in either back site. Mice were culled and biopsies taken from the ear, back and foot sites and fixed in 3.7% formol saline. Biopsies were embedded, sectioned and stained with Haemotoxylin and eosin. Sites injected with muKS1a had a marked increase in polymorphonuclear granulocytes, whereas sites injected with phosphate buffered saline had a low background infiltrate of polymorphonuclear granulocytes.

Chemokines are a large superfamily of highly basic secreted proteins with a broad number of functions (Baggiolini *et al.*, *Annu. Rev. Immunol.* 15:675-705, 1997; Ward *et al.*, *Immunity* 9:1-11, 1998; Horuk, *Nature* 393:524-525, 1998). The polypeptide sequences of muKS1 and huKS1 have similarity to CXC chemokines, suggesting that this protein will act like other CXC chemokines. The *in vivo* data from nude mice supports this hypothesis. This chemokine-like protein may therefore be expected to stimulate leukocyte, epithelial, stromal and neuronal cell migration, promote angiogenesis and vascular development, promote neuronal patterning, hematopoietic stem cell mobilization, keratinocyte and epithelial stem cell patterning and development, activation and proliferation of leukocytes, and promotion of migration in wound healing events. It has recently been shown that receptors to chemokines act as co-receptors for HIV-1 infection of CD4+ cells (Cairns *et al.*, *Nature Medicine* 4:563-568, 1998) and that high circulating levels of chemokines can render a degree of immunity to those exposed to the HIV virus (Zagury *et al.*, *Proc. Natl. Acad. Sci. USA* 95:3857-3861, 1998). This novel gene and its encoded protein may thus be usefully employed as regulators of epithelial, lymphoid, myeloid, stromal and neuronal cells migration and cancers; as agents for the treatment of cancers, neuro-degenerative diseases, inflammatory autoimmune diseases such as psoriasis, asthma and Crohns disease; for use in wound healing; and as agents for the prevention of HIV-1 binding and infection of leukocytes.

SEQ ID NOS: 1-72 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

While in the foregoing specification this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details

described herein may be varied considerably without departing from the basic principles of the invention.



We claim:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of: (1) sequences recited in SEQ ID NOS: 1-35; (2) complements of the sequences recited in SEQ ID NOS: 1-35; (3) reverse complements of the sequences recited in SEQ ID NOS: 1-35; (4) reverse sequences of the sequences recited in SEQ ID NOS: 1-35 (5) sequences having at least a 99% probability of being the same as a sequence recited in (1) – (4) above as determined using computer algorithm BLASTN; (6) sequences having at least 50% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (7) sequences having at least 75% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (8) sequences having at least 90% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (9) sequences having at least 95% identity to a nucleotide sequence recited in (1) – (4) above determined using computer algorithm BLASTN; (10) nucleotide sequences that hybridize to a sequence recited in (1) – (4) above under stringent hybridization conditions; (11) nucleotide sequences that are 200-mers of a sequence recited in (1) – (4) above; (12) nucleotide sequences that are 100-mers of a sequence recited in (1) – (4) above; (13) nucleotide sequences that are 40-mers of a sequence recited in (1) – (4) above; (14) nucleotide sequences that are 20-mers of a sequence recited in (1) – (4) above; and (15) nucleotide sequences that are degeneratively equivalent to a sequence recited in (1) – (4) above.

2. An oligonucleotide comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in claim 1.

3. A genetic construct comprising an isolated polynucleotide of claim 1.

4. A host cell transformed with a genetic construct of claim 3.

5. An isolated polypeptide encoded by a polynucleotide of claim 1.

5           6. An isolated polypeptide comprising an amino acid sequence  
selected from the group consisting of: (a) sequences provided in SEQ ID NOS:  
36-65; (b) sequences having at least a 99% probability of being the same as a  
sequence of SEQ ID NOS: 36-65, as determined using the computer algorithm  
BLASTP; (c) sequences having at least 50% identity to a sequence provided in  
10 SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP; (d)  
sequences having at least 75% identity to a sequence provided in SEQ ID NOS:  
36-65, as determined using the computer algorithm BLASTP; (e) sequences  
having at least 90% identity to a sequence provided in SEQ ID NOS: 36-65, as  
determined using the computer algorithm BLASTP; and (f) sequences having at  
15 least 95% identity to a sequence provided in SEQ ID NOS: 36-65, as determined  
using the computer algorithm BLASTP.

7. An isolated polynucleotide encoding a polypeptide of claim 6.

20           8. An isolated polypeptide comprising at least a functional portion of  
a polypeptide comprising an amino acid sequence selected from the group  
consisting of: (a) sequences provided in SEQ ID NOS: 36-65; (b) sequences  
having at least a 99% probability of being the same as a sequence of SEQ ID  
NOS: 36-65, as determined using the computer algorithm BLASTP; (c) sequences  
25 having at least 50% identity to a sequence provided in SEQ ID NOS: 36-65, as  
determined using the computer algorithm BLASTP; (d) sequences having at least  
75% identity to a sequence provided in SEQ ID NOS: 36-65, as determined using  
the computer algorithm BLASTP; (e) sequences having at least 90% identity to a  
sequence provided in SEQ ID NOS: 36-65, as determined using the computer  
30 algorithm BLASTP and (f) sequences having at least 95% identity to a sequence

provided in SEQ ID NOS: 36-65, as determined using the computer algorithm BLASTP.

5           9.     A composition comprising a polypeptide according to any one of claims 6 and 8 and at least one component selected from the group consisting of: physiologically acceptable carriers and immunostimulants.

10           10.    A composition comprising a polynucleotide according to claim 1 and at least one component selected from the group consisting of pharmaceutically acceptable carriers and immunostimulants.

          11.    A method for treating a disorder in a mammal comprising administering a composition according to claim 9.

15           12.    A method for treating a disorder in a mammal comprising administering a composition according to claim 10.

20           13.    A diagnostic kit comprising at least one oligonucleotide according to claim 2.

          14.    An organism comprising a host cell according to claim 4.

## SEQUENCE LISTING

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&lt;211&gt; 2515

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 4

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&lt;210&gt; 5

&lt;211&gt; 1587

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 5

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&lt;210&gt; 6

&lt;211&gt; 2494

&lt;212&gt; DNA

&lt;213&gt; Rat

&lt;400&gt; 6

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&lt;210&gt; 7

&lt;211&gt; 1859

&lt;212&gt; DNA



&lt;213&gt; Mouse

&lt;400&gt; 7

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&lt;210&gt; 8

&lt;211&gt; 2305

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 8

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&lt;210&gt; 10

&lt;211&gt; 2617

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 10

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&lt;210&gt; 9

&lt;211&gt; 1930

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 9

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&lt;213&gt; Mouse

&lt;400&gt; 13

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&lt;210&gt; 14

&lt;211&gt; 915

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 14

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&lt;210&gt; 15

&lt;211&gt; 1308

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 15

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&lt;210&gt; 16

&lt;211&gt; 1288

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 16

gctccagctc	ctccatcctg	tagtttacag	ggtgtaccct	atgtcgggac	caatgtgacc	60
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&lt;210&gt; 17

&lt;211&gt; 999

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 17

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ctcctgtgat	tccttttttcc	taaaaaaaa	aaaaaaaa			999

&lt;210&gt; 18

&lt;211&gt; 2123

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 18

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acttttaaaa	aaaaaaaaaa	aaa				2123

&lt;210&gt; 19

&lt;211&gt; 1391

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 19

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aaaaaaaaaa	a					1391

&lt;210&gt; 20

&lt;211&gt; 1864

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 20

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aaaa						1864

&lt;210&gt; 21

&lt;211&gt; 2324

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 21

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&lt;210&gt; 22

&lt;211&gt; 1859

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 22

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&lt;210&gt; 25

&lt;211&gt; 881

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 25

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&lt;210&gt; 26

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 26

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&lt;210&gt; 27

&lt;211&gt; 750

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 27

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&lt;210&gt; 28

&lt;211&gt; 1896

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 28

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&lt;210&gt; 29

&lt;211&gt; 1854

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 29

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&lt;210&gt; 30

&lt;211&gt; 2866

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 30

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ttgtagttgt	ctttctgagg	ctgacctgag	ttctctgata	ccattctctc	cagttgtatc	2220
cagtttcctg	taaacaatgt	gactttgttt	ttctcagtag	ctaaaacatc	ccaattatgt	2280
gagtgtacac	tttctttact	cattcctctg	tggggccacca	gctgggttgg	ttccatctct	2340
gagctattgt	gcattggaatt	gtctctgtgg	tgggtttagt	aaactcccag	gaatgcctgt	2400
acatgtttgt	agaggccaga	agaaggcaca	aaatcttgag	ccaggcttac	atgcacttgt	2460
gagtagcccc	acataggtgc	taagaaccca	gttcagggtcc	tctgctgtgg	gatgggtgggc	2520
tgtgcacaga	aagcctggtc	ccggtctagc	aaaggtctgg	aactccggag	ccggtgggct	2580
gtgattttaca	ccagcatggg	atggaaggag	ttggacctcg	cctcctgggc	acctggctcc	2640
tgtcacatag	ctacagcctc	ccacagcccc	cctatagggg	ggtagtcagc	atcaatcaca	2700
tagtagctgc	actaagccct	cccacatgca	aataagggtt	ccccaaactc	tcagtccaag	2760
ccaatgaaaa	gtacctgctg	tcaaacccta	aatcatcccc	aaaactctgt	aagtcctatc	2820
agggaataaa	atgtgtgtga	aaactaaaaa	aaaaaaaaaa	aaaaaa		2866

&lt;210&gt; 31

&lt;211&gt; 1093

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 31

gcgaccactg	agaccttgag	actcagacac	caagagagat	gtttctagtt	gggagcctcg	60
ttgtcctctg	tgggctgctg	gcccacagca	cagcacagct	ggcaggcttg	ccattgcccc	120
tggggccagg	tccacccttg	ccactgaacc	agggcccacc	gttgccactg	aaccagggcc	180
agctgttgcc	cctggctcag	gggtctgcct	tggctgtaag	cccagcactg	ccttcaaate	240
ccacagatct	tcttgctgga	aaattcacag	atgctctcag	cggtggcctg	ctgtctgggg	300
ggctgctggg	catttttgaa	aatattccac	tcttgatgtg	tataaagtct	ggaggaggca	360
attctaattg	ccttggttgg	ggcctgctgg	gaaaactgac	gtcatcagtt	cctctcctga	420
acaacatcct	cgacataaaa	atcactgato	cgcagctgct	agaacttggg	cttgtgcaga	480
gtcctgatgg	ccatcgtctc	tatgtcacca	tccctctggg	cttgacactc	aacgtaaata	540
tgcccgtagt	tgggaagtct	ttgcaattgg	ctgtgaagct	gaacattact	gcagaagtct	600
tagccgtgaa	agacaatcag	gggaggattc	atctggttct	tgggtgactgc	accactccc	660
ctggcagcct	gaaaatcagc	ttgctcaatg	gagtcactcc	tgttcaaagc	tttttagaca	720
acctcacagg	gatattgact	aaagtccctc	ctgagctgat	ccagggcaag	gtatgtcctc	780
tgggtcaatg	gattctcagc	ggtttggatg	tcaccctggg	gcacaacatt	gctgaattac	840
tgatccatgg	actacagttt	gtcatcaaag	tttaggcata	ccaggaagga	aggctatott	900
ggctgagctg	aatcattttc	tgctgctcag	tctcctgcct	cttgcccagt	ctcccatggc	960
tcacagaaaag	ggggccacat	cctggaaaaat	tatgtcttcc	ttctcctcac	ggagcctgat	1020
ctcttcccat	caggcacgat	taatcctgtg	atcctcacta	aataaaatag	ctcttcatct	1080
gcaaaaaaaaa	aaa					1093

&lt;210&gt; 32

<211> 1353  
 <212> DNA  
 <213> Mouse

<400> 32  
 gaaacagtat gagcaaacac tgagctgagg ggagcttctg attaagagcg ctccccagcg 60  
 agggccgagg ccgtgaacct tcccagcaag aggggtggtg ttgctcctgg aagcctgcgc 120  
 ccagcagctg aagccatggc caccaccacg tgccagggtg tagggcttct cctgtccctc 180  
 ctgggtctgg ccggctgcat agccgccact gggatggaca tgtggagcac tcaagacctg 240  
 tatgacaacc cagtaccgcg cgtgttccag catgaagggc tctggaggag ttgctgcaa 300  
 cagagctcgg ggttcaccga gtgccggcca tacttcacca tcctgggcct tccagccatg 360  
 ctgcaagctg tacgagccct gatgatcgtg ggcattgttc tgggggtcat cggtatcctc 420  
 gtgtccatct tcgccctgaa gtgcattcgc attggtagca tggatgactc tgccaaggcc 480  
 aagatgactc tgacttctgg gatcttggtc atcatctccg gcatctgtgc aatcattggt 540  
 gtgtctgtgt ttgccaacat gctgggtgac aacttctgga tgtccacagc taacatgtac 600  
 agcggcatgg gcggcatggg tggcatggtg cagaccgttc agaccaggta caccttcggt 660  
 gcagctctgt tcgtgggctg ggttgctgga ggcctcacc tgattggggg agtgatgatg 720  
 tgcacgcct gccgtggcct gacaccagat gacagcaact tcaaagctgt gtcttaccat 780  
 gcctctggcc aaaatgttgc ctacaggcct ggaggcttta aggccagcac tggctttggg 840  
 tccaacacca gaaacaagaa gatctacgat gggggtgccc gcacagaaga cgatgaacag 900  
 tctcatccta ccaagtatga ctatgtgtag tgctctaaga ccgcgaacc tgtgtgcagg 960  
 aggaaccctt cccaagaag agctcaccgc aaagcaacgg gagtctacct tgttcccttg 1020  
 ttgatttcaa ctgacatctg aaagtggta aagcctgatt ttcattccata gggaggctag 1080  
 acagtcttgg ccacatgtgt ctgcctctaa atatcccatc acaaaacagc tgagttatcg 1140  
 tttatgagtt agaggccata aactcactt tagcccaacc ctctgctttt taccgtagac 1200  
 tttcttttca tctggtgatg gaatggaatt tgactcacag actaatactt taatggttta 1260  
 gagaaacttt ccttcctcgt acttaataag cctgctgatg gtcgattttc cagcttgacc 1320  
 accaagggaa attttaaaaa aaaaaaaaaa aaa 1353

<210> 33  
 <211> 1046  
 <212> DNA  
 <213> Mouse

<400> 33  
 gcctcagtcc acagctgtct cccagctgc ttccagtga cccccggca gtctaggctc 60  
 ccacagcaat gagggtggtg agggacaact tctggatcat cttagctatg tccatcatct 120  
 tcatctccct ggtcctgggt ctcatcctgt actgtgtctg cagggtggcag cttagacaag 180  
 gcaggaactg ggaattgct aagccctcaa aacaggatgg aagagatgaa gaaaagatgt 240  
 atgagaatgt tcttaattct tcaccaggcc agttacctgc tctgccacc aggggttcac 300  
 cttttccagg agacctagcc ccacaggaag ctccaagaca accctcagct tggtagctat 360  
 cagtgaagaa agttaggaac aagaaggctt ttgctatctc gggctccacc gagccagaaa 420  
 atgattatga tgatgttgag attccagcaa ccaccgaaac ccagcactct aaaaccacac 480  
 ctttttggca agctgaagtg ggtttacaca gctcgtttta gaatactcta gaatagccgg 540  
 attataacac aagcacttcc taatccccag aggaagccac ctgagccatg tgaagctac 600  
 agcagaagac aggacagctt gatgttcccg aggtccaga tgtttctgtt gctccagatg 660  
 tttctgctgc tccagatggt tctgttgctc caaatatttc tgctgctcca gatgtttctg 720  
 ttgtccaga tgtttctgtt gctccagatg ctctgttgcc tccagatgct cctgatgttt 780  
 ctgacactgc agaagctcta cccaagatt ctgaggatgt ggccttggca cctttgtgga 840  
 ggaagtttcc ttagtgacaga ccactgggcc tgtgagaact gactcatttc tcaacatttt 900  
 ctttcgttcc ctgggtgaat gtagctgtaa ggcagtgact ctcaaccttc ctaatgcagg 960  
 gatccttcaa tacaattcct tatttggtgt gatcctcaac cataaaatta ttttgttgct 1020  
 acttcaaaaa aaaaaaaaaa aaaaaa 1046

<210> 34  
 <211> 1261  
 <212> DNA



&lt;213&gt; Mouse

&lt;400&gt; 34

```

gcacagacgg gtaaaccgct tgggaacctc gaggaaaaag aggtaacgaa aaccttttcc      60
taagaggcta caaatTTTgga agcagggaaa acccagacat gagatgtttt tagtttattt    120
ctccagaagg gggcactgta tcaattatgt gaaggacat gcagacagcc tagctccatg    180
gtgctgtggg gtaggactga ggagccctct ggccagaccc cagcacggcc atgtctctcc    240
caaggatcat gttcctggag gtcacgcccc tggtccttct cataagtggc tgtgcacagc    300
agctctctgg aggtatttgg aacattctgc tgtcacacat gggactgctc ttcctgaagc    360
ccacgctgtt cgtgggaaac atgggaagaa aggaagacgt gttgtgtgct gctcagtaga    420
cttcccacaa gccacctctc tcttctgaaa cgtcactgaa tggactggag aggactgcgg    480
gtttataaaa ctgcttttta tctgagaaca atgggtttgg aaactagtct cttttcttcc    540
cactttttaca gagcttctca aatcattcct ccaggccctg acttggacag gtagggggggc    600
agaccctggg toccaagggt cactgtccag gcacactgcc cacattgcta agagaagagg    660
ccctgctgcc agtggaccct tcacccca cagacacct gtcttgctt taggacaccc    720
tcctctagag agtgggtgtg gaaggagggg acctatgtaa ggagttgggg caggcatgaa    780
tctgccaaat actggatatg gatccaaggc tggcccaggc acctgcacct ccagtgagtg    840
gtcagcaggt ggcgctgctg ccgcccaggc ttcacagagt ccctttaggg agtctgctcc    900
cagatccctt ctggtgcaca cttactggat gtactgcaa gctctaccct ctgagcaggt    960
gttgcaccac agtggcgctg accctggccc cgcaacggca actgctgaag gcagccattg   1020
cctcagccat tctcaagacc cttcaatttt taaaagcagt tcgattctgt aatatttatt   1080
tttctttttg aggatgttct gttgcccgcg agactgactg cagtgtgcac cattgcatga   1140
gccctgcctc agtgccctgt ggctccctgg gcactgctgc ccctctgtct aaagctgact   1200
gtggcagcac tgcccaacaa taaagctgac ctaaaagctg aaaaaaaaaa aaaaaaaaaa   1260
a                                                    1261

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&lt;210&gt; 35

&lt;211&gt; 995

&lt;212&gt; DNA

&lt;213&gt; Mouse

&lt;400&gt; 35

```

gtcaccgccg gtccggggcg ggcgaggccc cgtctccttg ccttccaggc ctcatgcgct      60
cccgcgcctg gctccgcgca ccgctgcccg gagggagggg gcccgcttg tctgcgcgtc    120
taocgaggcc tcataggcac cgtgggtcac cccaactacc tggacaacgt gagegcgcgc    180
gttgcgcctt ggtgcggctg tgcggccagt ggaaaccggc gcgaagaatg cgaagccttc    240
cgcaagctct ttacaaggaa cccctgcttg gatggtgcc aacaagcctt tgacagcttg    300
cagccatcag ttctgcagga ccagactgct ggggtgctgt tcccgcgggt gtcctggctg    360
tatgactca ctgccctggc tctccaggcc ctgctctgat taggaacatg aaccgtggac    420
gacacagctg actgccatgt ctcccgatga ctgctcactg agctgaaact cccttgccct    480
caggctctgt gccctttgca ggccctggacc cttgtgtggc tgtcctctgg attgggggct    540
ggaggctagg gtctgactga aaagcctgtg ttcccctgtc agtaggcac ttgtccgttt    600
tcttccccat cctagagctg agcaccata gatgaggcct cattgggtcc cctgggctta    660
cagagcagga cagagactag cccccgctcc tagaattcgg aactgtcctt ttccaagatg    720
acaaggcact aaggagatca tatgaacagg ctgacagaca aggctgccta aataccctcc    780
cagttagcca ttattcacca ttaagcttac ccgtgtcaca gcactgacgt ggcttgtcac    840
ctatgacaca gtgtgtagac attaaggaga gactgaggtc cctcctgctc agcacccac    900
tggcttccca ggctttccct gccatgggtt ccccgagcacc tgcaggggct caataaaccc    960
atgtgcactg agaaaaaaaa aaaaaaaaaa aaaaaa

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&lt;210&gt; 36

&lt;211&gt; 747

&lt;212&gt; PRT

&lt;213&gt; Rat

&lt;400&gt; 36

Glu Ala Thr Val Ile Thr Thr Glu Lys Arg Glu Arg Pro Ala Pro Pro

1	5	10	15
Arg Glu Leu Leu Val Pro Gln Ala Glu Val Thr Ala Arg Ser Leu Arg			
20		25	30
Leu Gln Trp Val Pro Gly Ser Asp Gly Ala Ser Pro Ile Arg Tyr Phe			
35	40	45	
Thr Val Gln Val Arg Glu Leu Pro Gly Gly Glu Trp Gln Thr Tyr Ser			
50	55	60	
Ser Ser Ile Ser His Glu Ala Thr Leu Cys Ala Val Glu Arg Leu Arg			
65	70	75	80
Pro Phe Thr Ser Tyr Lys Leu Arg Leu Lys Ala Thr Asn Asp Ile Gly			
85	90	95	
Asp Ser Asp Phe Ser Ala Glu Thr Glu Ala Val Thr Thr Leu Gln Asp			
100	105	110	
Val Pro Gly Glu Pro Pro Gly Ser Val Ser Ala Thr Pro His Thr Thr			
115	120	125	
Ser Ser Val Leu Ile Gln Trp Gln Pro Pro Arg Asp Glu Ser Leu Asn			
130	135	140	
Gly Leu Leu Gln Gly Tyr Arg Ile Tyr Tyr Arg Glu Leu Glu Ser Glu			
145	150	155	160
Thr Gly Leu Ser Pro Glu Pro Lys Thr Leu Lys Ser Pro Ser Ala Leu			
165	170	175	
Arg Ala Glu Leu Thr Ala Gln Ser Ser Phe Lys Thr Val Asn Ser Ser			
180	185	190	
Ser Thr Leu Thr Thr Tyr Glu Leu Thr His Leu Lys Lys Tyr Arg Arg			
195	200	205	
Tyr Glu Val Ile Met Thr Ala Tyr Asn Ile Ile Gly Glu Ser Pro Ala			
210	215	220	
Ser Val Pro Val Glu Val Phe Val Gly Glu Ala Ala Pro Ala Met Ala			
225	230	235	240
Pro Gln Asn Ile Gln Val Thr Pro Leu Thr Ala Ser Gln Leu Glu Val			
245	250	255	
Thr Trp Asp Pro Pro Pro Pro Glu Ser Gln Asn Gly Asn Ile Gln Gly			
260	265	270	
Tyr Lys Val Tyr Tyr Trp Glu Ala Asp Ser Arg Asn Glu Thr Glu Lys			
275	280	285	
Met Lys Val Leu Phe Leu Pro Glu Pro Val Val Lys Ile Lys Asp Leu			
290	295	300	
Thr Ser His Thr Lys Tyr Leu Val Ser Ile Ser Ala Phe Asn Ala Ala			
305	310	315	320
Gly Asp Gly Pro Arg Ser Asp Pro Cys Gln Gly Arg Thr His Gln Ala			
325	330	335	
Ala Pro Gly Pro Pro Ser Phe Leu Glu Phe Ser Glu Ile Thr Ser Thr			
340	345	350	
Thr Leu Asn Val Ser Trp Gly Glu Pro Ser Ala Ala Asn Gly Ile Leu			
355	360	365	
Gln Gly Tyr Arg Val Val Tyr Glu Pro Leu Ala Pro Val Gln Gly Val			
370	375	380	
Ser Lys Val Val Thr Val Asp Val Lys Gly Asn Trp Gln Arg Trp Leu			
385	390	395	400
Lys Val Arg Asp Leu Thr Lys Gly Val Thr Tyr Phe Phe Arg Val Gln			
405	410	415	
Ala Arg Thr Ile Ala Tyr Gly Pro Glu Leu Gln Ala Asn Val Thr Ala			
420	425	430	
Gly Pro Ala Glu Gly Ser Pro Gly Ser Pro Arg Asn Val Leu Val Thr			
435	440	445	
Lys Ser Ala Ser Glu Leu Thr Leu Gln Trp Thr Glu Gly Asn Thr Gly			
450	455	460	

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Asn Thr Pro Thr Thr Gly Tyr Val Ile Glu Ala Arg Pro Ser Asp Glu
465          470          475          480
Gly Leu Trp Asp Met Phe Ala Lys Asp Ile Pro Arg Ser Ala Thr Ser
          485          490          495
Tyr Thr Val Gly Leu Asp Lys Leu Arg Gln Gly Val Thr Tyr Glu Phe
          500          505          510
Arg Val Val Ala Val Asn Lys Ala Gly Phe Gly Glu Pro Ser Arg Pro
          515          520          525
Ser Ile Ala Val Ser Ala Gln Ala Glu Ala Pro Phe Tyr Glu Glu Trp
          530          535          540
Trp Phe Leu Leu Val Ile Ala Leu Ser Ser Leu Leu Val Leu Leu
545          550          555          560
Val Val Phe Val Leu Val Leu His Gly Gln Ser Lys Lys Tyr Lys Asn
          565          570          575
Cys Gly Ser Gly Lys Gly Ile Ser Asn Met Glu Glu Thr Val Thr Leu
          580          585          590
Asp Asn Gly Gly Phe Ala Ala Leu Glu Leu Asn Ser Arg His Leu Asn
          595          600          605
Val Lys Ser Thr Phe Ser Lys Lys Asn Gly Thr Arg Ser Pro Pro Arg
          610          615          620
Pro Ser Pro Gly Gly Leu His Tyr Ser Asp Glu Asp Ile Cys Asn Lys
625          630          635          640
Tyr Asn Gly Ala Val Leu Thr Glu Ser Val Asn Leu Lys Glu Lys Ser
          645          650          655
Val Asp Gly Ser Glu Ser Glu Ala Ser Asp Ser Asp Tyr Glu Glu Ala
          660          665          670
Leu Pro Lys His Ser Phe Val Asn His Tyr Met Ser Asp Pro Thr Tyr
          675          680          685
Tyr Asn Phe Trp Lys Arg Arg Pro Pro Ala Ala Ala Pro His Arg Tyr
690          695          700
Glu Ala Val Ala Gly Ala Glu Ala Gly Pro His Leu His Thr Val Ile
705          710          715          720
Thr Thr Gln Ser Ala Gly Gly Val Tyr Thr Pro Ala Gly Pro Gly Ala
          725          730          735
Arg Ala Pro Leu Thr Gly Phe Ser Ser Phe Val
          740          745

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<210> 37  
 <211> 205  
 <212> PRT  
 <213> Mouse

```

<400> 37
Met Leu Gly Thr Leu Val Trp Met Leu Ala Val Gly Phe Leu Leu Ala
1          5          10          15
Leu Ala Pro Gly Arg Ala Ala Gly Ala Leu Arg Thr Gly Arg Arg Pro
          20          25          30
Ala Arg Pro Arg Asp Cys Ala Asp Arg Pro Glu Glu Leu Leu Glu Gln
          35          40          45
Leu Tyr Gly Arg Leu Ala Ala Gly Val Leu Ser Ala Phe His His Thr
          50          55          60
Leu Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala
65          70          75          80
Gly Gly Arg Ala Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg
          85          90          95
Ser Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Phe
          100          105          110

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Pro Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr  
 115 120 125  
 Gly Leu Tyr Gly Glu Glu Asp Phe Arg Phe Arg Ser Thr Pro Val Phe  
 130 135 140  
 Ser Pro Ala Val Val Leu Arg Arg Thr Ala Ala Cys Ala Gly Gly Arg  
 145 150 155 160  
 Ser Val Tyr Ala Glu His Tyr Ile Thr Ile Pro Val Gly Cys Thr Cys  
 165 170 175  
 Val Pro Glu Pro Asp Lys Ser Ala Asp Ser Ala Asn Ser Ser Met Asp  
 180 185 190  
 Lys Leu Leu Leu Gly Pro Ala Asp Arg Pro Ala Gly Arg  
 195 200 205

<210> 38  
 <211> 238  
 <212> PRT  
 <213> Mouse

<400> 38  
 Met Leu Cys Phe Leu Arg Gly Met Ala Phe Val Pro Phe Leu Leu Val  
 1 5 10 15  
 Thr Trp Ser Ser Ala Ala Phe Ile Ile Ser Tyr Val Val Ala Val Leu  
 20 25 30  
 Ser Gly His Val Asn Pro Phe Leu Pro Tyr Ile Ser Asp Thr Gly Thr  
 35 40 45  
 Thr Pro Pro Glu Ser Gly Ile Phe Gly Phe Met Ile Asn Phe Ser Ala  
 50 55 60  
 Phe Leu Gly Ala Ala Thr Met Tyr Thr Arg Tyr Lys Ile Val Glu Lys  
 65 70 75 80  
 Gln Asn Glu Thr Cys Tyr Phe Ser Thr Pro Val Phe Asn Leu Val Ser  
 85 90 95  
 Leu Ala Leu Gly Leu Val Gly Cys Ile Gly Met Gly Ile Val Ala Asn  
 100 105 110  
 Phe Gln Glu Leu Ala Val Pro Val Val His Asp Gly Gly Ala Leu Leu  
 115 120 125  
 Ala Phe Val Cys Gly Val Val Tyr Thr Leu Leu Gln Ser Ile Ile Ser  
 130 135 140  
 Tyr Lys Ser Cys Pro Gln Trp Asn Ser Leu Thr Thr Cys His Val Arg  
 145 150 155 160  
 Met Ala Ile Ser Ala Val Ser Cys Ala Ala Val Val Pro Met Ile Ala  
 165 170 175  
 Cys Ala Ser Leu Ile Ser Ile Thr Lys Leu Glu Trp Asn Pro Lys Glu  
 180 185 190  
 Lys Asp Tyr Ile Tyr His Val Val Ser Ala Ile Cys Glu Trp Thr Val  
 195 200 205  
 Ala Phe Gly Phe Ile Phe Tyr Phe Leu Thr Phe Ile Gln Asp Phe Gln  
 210 215 220  
 Ser Val Thr Leu Arg Ile Ser Thr Glu Ile Asn Asp Asp Phe  
 225 230 235

<210> 39  
 <211> 492  
 <212> PRT  
 <213> Mouse

<400> 39  
 Leu Arg Leu Leu Leu Ala Trp Val Ala Ala Val Pro Ala Leu Gly Gln

1	5	10	15
Val Pro Trp Thr	Pro Glu Pro Arg	Ala Cys Gly Pro	Ser Ser Cys
	20	25	30
Tyr Ala Leu Phe	Pro Arg Arg Arg	Thr Phe Leu Glu	Ala Trp Arg Ala
	35	40	45
Cys Arg Glu Leu	Gly Gly Asn Leu	Ala Thr Pro Arg	Thr Pro Glu Glu
	50	55	60
Ala Gln Arg Val	Asp Ser Leu Val	Gly Val Gly Pro	Ala Asn Gly Leu
	65	70	75
Leu Trp Ile Gly	Leu Gln Arg Gln	Ala Arg Gln Cys	Gln Pro Gln Arg
	85	90	95
Pro Leu Arg Gly	Phe Ile Trp Thr	Thr Gly Asp Gln	Asp Thr Ala Phe
	100	105	110
Thr Asn Trp Ala	Gln Pro Ala Thr	Glu Gly Pro Cys	Pro Ala Gln Arg
	115	120	125
Cys Ala Ala Leu	Glu Ala Ser Gly	Glu His Arg Trp	Leu Glu Gly Ser
	130	135	140
Cys Thr Leu Ala	Val Asp Gly Tyr	Leu Cys Gln Phe	Gly Phe Glu Gly
	145	150	155
Ala Cys Pro Ala	Leu Pro Leu Glu	Val Gly Gln Ala	Gly Pro Ala Val
	165	170	175
Tyr Thr Thr Pro	Phe Asn Leu Val	Ser Ser Glu Phe	Glu Trp Leu Pro
	180	185	190
Phe Gly Ser Val	Ala Ala Val Gln	Cys Gln Ala Gly	Arg Gly Ala Ser
	195	200	205
Leu Leu Cys Val	Lys Gln Pro Ser	Gly Gly Val Gly	Trp Ser Gln Thr
	210	215	220
Gly Pro Leu Cys	Pro Gly Thr Gly	Cys Gly Pro Asp	Asn Gly Gly Cys
	225	230	235
Glu His Glu Cys	Val Glu Glu Val	Asp Gly Ala Val	Ser Cys Arg Cys
	245	250	255
Ser Glu Gly Phe	Arg Leu Ala Ala	Asp Gly His Ser	Cys Glu Asp Pro
	260	265	270
Cys Ala Gln Ala	Pro Cys Glu Gln	Gln Cys Glu Pro	Gly Gly Pro Gln
	275	280	285
Gly Tyr Ser Cys	His Cys Arg Leu	Gly Phe Arg Pro	Ala Glu Asp Asp
	290	295	300
Pro His Arg Cys	Val Asp Thr Asp	Glu Cys Gln Ile	Ala Gly Val Cys
	305	310	315
Gln Gln Met Cys	Val Asn Tyr Val	Gly Gly Phe Glu	Cys Tyr Cys Ser
	325	330	335
Glu Gly His Glu	Leu Glu Ala Asp	Gly Ile Ser Cys	Ser Pro Ala Gly
	340	345	350
Ala Met Gly Ala	Gln Ala Ser Gln	Asp Leu Arg Asp	Glu Leu Leu Asp
	355	360	365
Asp Gly Glu Glu	Gly Glu Asp Glu	Glu Glu Pro Trp	Glu Asp Phe Asp
	370	375	380
Gly Thr Trp Thr	Glu Glu Gln Gly	Ile Leu Trp Leu	Ala Pro Thr His
	385	390	395
Pro Pro Asp Phe	Gly Leu Pro Tyr	Arg Pro Asn Phe	Pro Gln Asp Gly
	405	410	415
Glu Pro Gln Arg	Leu His Leu Glu	Pro Thr Trp Pro	Pro Pro Leu Lys
	420	425	430
Ala Pro Lys Gly	Pro Gln Gln Pro	Pro Arg Gly Ala	Ala Lys Thr Pro
	435	440	445
Lys Gly Asn Pro	Ala Asn Pro Thr	His Thr Thr Phe	Cys Pro Gln Asp
	450	455	460

Leu Cys Tyr Phe Ser Tyr Thr Pro Thr Pro Glu Pro Cys Pro Pro Thr  
 465 470 475 480  
 Cys His Gly Pro Cys His Thr Ser Ser Cys Val Leu  
 485 490

<210> 40  
 <211> 464  
 <212> PRT  
 <213> Mouse

<400> 40

Met Gly Arg Ala Trp Gly Leu Leu Val Gly Leu Leu Gly Val Val Trp  
 1 5 10 15  
 Leu Leu Arg Leu Gly His Gly Glu Glu Arg Arg Pro Glu Thr Ala Ala  
 20 25 30  
 Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp Cys Thr Cys  
 35 40 45  
 Asp Val Glu Thr Ile Asp Lys Phe Asn Asn Tyr Arg Leu Phe Pro Arg  
 50 55 60  
 Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg Tyr Tyr Lys Val Asn  
 65 70 75 80  
 Leu Lys Lys Pro Cys Pro Phe Trp Asn Asp Ile Asn Gln Cys Gly Arg  
 85 90 95  
 Arg Asp Cys Ala Val Lys Pro Cys His Ser Asp Glu Val Pro Asp Gly  
 100 105 110  
 Ile Lys Ser Ala Ser Tyr Lys Tyr Ser Glu Glu Ala Asn Arg Ile Glu  
 115 120 125  
 Glu Cys Glu Gln Ala Glu Arg Leu Gly Ala Val Asp Glu Ser Leu Ser  
 130 135 140  
 Glu Glu Thr Gln Lys Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser  
 145 150 155 160  
 Ser Asp Ser Phe Cys Glu Ile Asp Asp Ile Gln Ser Pro Asp Ala Glu  
 165 170 175  
 Tyr Val Asp Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly  
 180 185 190  
 Pro Asp Ala Trp Arg Ile Trp Ser Val Ile Tyr Glu Glu Asn Cys Phe  
 195 200 205  
 Lys Pro Gln Thr Ile Gln Arg Pro Leu Ala Ser Gly Arg Gly Lys Ser  
 210 215 220  
 Lys Glu Asn Thr Phe Tyr Asn Trp Leu Glu Gly Leu Cys Val Glu Lys  
 225 230 235 240  
 Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His Ala Ser Ile Asn Val  
 245 250 255  
 His Leu Ser Ala Arg Tyr Leu Leu Gln Asp Thr Trp Leu Glu Lys Lys  
 260 265 270  
 Trp Gly His Asn Val Thr Glu Phe Gln Gln Arg Phe Asp Gly Ile Leu  
 275 280 285  
 Thr Glu Gly Glu Gly Pro Arg Arg Leu Arg Asn Leu Tyr Phe Leu Tyr  
 290 295 300  
 Leu Ile Glu Leu Arg Ala Leu Ser Lys Val Leu Pro Phe Phe Glu Arg  
 305 310 315 320  
 Pro Asp Phe Gln Leu Phe Thr Gly Asn Lys Val Gln Asp Ala Glu Asn  
 325 330 335  
 Lys Ala Leu Leu Glu Ile Leu His Glu Ile Lys Ser Phe Pro Leu  
 340 345 350  
 His Phe Asp Glu Asn Ser Phe Phe Ala Gly Asp Lys Asn Glu Ala His  
 355 360 365

Lys Leu Lys Glu Asp Phe Arg Leu His Phe Arg Asn Ile Ser Arg Ile  
 370 375 380  
 Met Asp Cys Val Gly Cys Phe Lys Cys Arg Leu Trp Gly Lys Leu Gln  
 385 390 395 400  
 Thr Gln Gly Leu Gly Thr Ala Leu Lys Ile Leu Phe Ser Glu Lys Leu  
 405 410 415  
 Ile Ala Asn Met Pro Glu Ser Gly Pro Ser Tyr Glu Phe Gln Leu Thr  
 420 425 430  
 Arg Gln Glu Ile Val Ser Leu Phe Asn Ala Phe Gly Arg Ile Ser Thr  
 435 440 445  
 Ser Val Arg Glu Leu Glu Asn Phe Arg His Leu Leu Gln Asn Val His  
 450 455 460

<210> 41  
 <211> 148  
 <212> PRT  
 <213> Rat

<400> 41  
 Leu Asn Trp Gln Ile Lys Lys Tyr Asp Thr Lys Ala Ala Tyr Cys Gln  
 1 5 10 15  
 Ser Lys Leu Ala Val Val Leu Phe Thr Lys Glu Leu Ser Arg Arg Leu  
 20 25 30  
 Gln Gly Thr Gly Val Thr Val Asn Ala Leu His Pro Gly Val Ala Arg  
 35 40 45  
 Thr Glu Leu Gly Arg His Thr Gly Met His Asn Ser Ala Phe Ser Gly  
 50 55 60  
 Phe Met Leu Gly Pro Phe Phe Trp Leu Leu Phe Lys Ser Pro Gln Leu  
 65 70 75 80  
 Ala Ala Gln Pro Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Glu Ser  
 85 90 95  
 Val Ser Gly Lys Tyr Phe Asp Gly Leu Arg Glu Lys Ala Pro Ser Pro  
 100 105 110  
 Glu Ala Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Thr Glu Ser Ala  
 115 120 125  
 His Leu Val Gly Leu Asp Met Ala His Gly Ser Ser Gly Arg Gly His  
 130 135 140  
 Ser Ile Ser Arg  
 145

<210> 42  
 <211> 228  
 <212> PRT  
 <213> Mouse

<400> 42  
 Met Gly Phe Leu Leu Leu Leu Leu His Ala Ala Ile Ala Gly His  
 1 5 10 15  
 Lys Asn Tyr Gly Thr His Asn His Cys Trp Leu Ser Leu His Arg Gly  
 20 25 30  
 Phe Ile Trp Ser Phe Leu Gly Pro Ala Ala Ala Ile Ile Leu Ile Asn  
 35 40 45  
 Leu Val Phe Tyr Phe Leu Ile Trp Ile Leu Arg Ser Lys Leu Ser  
 50 55 60  
 Ser Leu Asn Lys Glu Val Ser Thr Leu Gln Asp Thr Lys Val Met Thr  
 65 70 75 80  
 Phe Lys Ala Ile Val Gln Leu Phe Val Leu Gly Cys Ser Trp Gly Ile

Met 1	Lys	Glu	Tyr	Val 5	Met	Leu	Leu	Leu	Leu 10	Ala	Val	Cys	Ser	Ala 15	Lys
Pro	Phe	Phe	Ser 20	Pro	Ser	His	Thr	Ala 25	Leu	Lys	Asn	Met 30	Met	Leu	Lys
Asp	Met	Glu 35	Asp	Thr	Asp	Asp	Asp 40	Asp	Asn	Asp	Asp 45	Asp	Asn	Ser	
Leu	Phe 50	Pro	Thr	Lys	Glu	Pro 55	Val	Asn	Pro	Phe 60	Phe	Pro	Phe	Asp	Leu
Phe 65	Pro	Thr	Cys	Pro	Phe 70	Gly	Cys	Gln	Cys	Tyr 75	Ser	Arg	Val	Val	His 80
Cys	Ser	Asp	Leu	Gly 85	Leu	Thr	Ser	Val	Pro 90	Asn	Asn	Ile	Pro	Phe 95	Asp
Thr	Arg	Met	Val 100	Asp	Leu	Gln	Asn	Asn 105	Lys	Ile	Lys	Glu 110	Ile	Lys	Glu
Asn	Asp	Phe 115	Lys	Gly	Leu	Thr	Ser 120	Leu	Tyr	Ala	Leu	Ile 125	Leu	Asn	Asn
Asn	Lys 130	Leu	Thr	Lys	Ile	His 135	Pro	Lys	Thr	Phe	Leu 140	Thr	Thr	Lys	Lys
Leu 145	Arg	Arg	Leu	Tyr	Leu 150	Ser	His	Asn	Gln	Leu 155	Ser	Glu	Ile	Pro	Leu 160
Asn	Leu	Pro	Lys	Ser 165	Leu	Ala	Glu	Leu	Arg 170	Ile	His	Asp	Asn	Lys	Val
Lys	Lys	Ile 180	Gln	Lys	Asp	Thr	Phe	Lys 185	Gly	Met	Asn	Ala 190	Leu	His	Val
Leu	Glu 195	Met	Ser	Ala	Asn	Pro	Leu 200	Glu	Asn	Asn	Gly 205	Ile	Glu	Pro	Gly
Ala	Phe 210	Glu	Gly	Val	Thr	Val 215	Phe	His	Ile	Arg	Ile 220	Ala	Glu	Ala	Lys
Leu 225	Thr	Ser	Ile	Pro	Lys 230	Gly	Leu	Pro	Pro	Thr 235	Leu	Leu	Glu	Leu	His 240
Leu	Asp	Phe	Asn	Lys	Ile	Ser	Thr	Val	Glu	Leu	Glu	Asp	Leu	Lys	Arg



[illegible]

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<210> 44
<211> 466
<212> PRT
<213> Mouse
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<400>	44															
Met	Trp	Gly	Cys	Trp	Leu	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Gly	Gln	
1				5					10					15		
Ala	Ala	Leu	Glu	Ala	Arg	Arg	Ser	Arg	Trp	Arg	Arg	Glu	Leu	Ala	Pro	
			20					25					30			
Gly	Leu	His	Leu	Arg	Gly	Ile	Arg	Asp	Ala	Gly	Gly	Arg	Tyr	Cys	Gln	
		35					40					45				
Glu	Gln	Asp	Met	Cys	Cys	Arg	Gly	Arg	Ala	Asp	Glu	Cys	Ala	Leu	Pro	
	50					55					60					
Tyr	Leu	Gly	Ala	Thr	Cys	Tyr	Cys	Asp	Leu	Phe	Cys	Asn	Arg	Thr	Val	
65					70					75					80	
Ser	Asp	Cys	Cys	Pro	Asp	Phe	Trp	Asp	Phe	Cys	Leu	Gly	Ile	Pro	Pro	
				85					90					95		
Pro	Phe	Pro	Pro	Val	Gln	Gly	Cys	Met	His	Gly	Gly	Arg	Ile	Tyr	Pro	
			100					105					110			
Val	Phe	Gly	Thr	Tyr	Trp	Asp	Asn	Cys	Asn	Arg	Cys	Thr	Cys	His	Glu	
		115					120					125				
Gly	Gly	His	Trp	Glu	Cys	Asp	Gln	Glu	Pro	Cys	Leu	Val	Asp	Pro	Asp	
		130				135					140					
Met	Ile	Lys	Ala	Ile	Asn	Arg	Gly	Asn	Tyr	Gly	Trp	Gln	Ala	Gly	Asn	
145					150					155					160	
His	Ser	Ala	Phe	Trp	Gly	Met	Thr	Leu	Asp	Glu	Gly	Ile	Arg	Tyr	Arg	
				165					170					175		
Leu	Gly	Thr	Ile	Arg	Pro	Ser	Ser	Thr	Val	Met	Asn	Met	Asn	Glu	Ile	
			180					185					190			
Tyr	Thr	Val	Leu	Gly	Gln	Gly	Glu	Val	Leu	Pro	Thr	Ala	Phe	Glu	Ala	
		195					200					205				
Ser	Glu	Lys	Trp	Pro	Asn	Leu	Ile	His	Glu	Pro	Leu	Asp	Gln	Gly	Asn	
	210					215					220					
Cys	Ala	Gly	Ser	Trp	Ala	Phe	Ser	Thr	Ala	Ala	Val	Ala	Ser	Asp	Arg	
225					230					235					240	
Val	Ser	Ile	His	Ser	Leu	Gly	His	Met	Thr	Pro	Ile	Leu	Ser	Pro	Gln	
				245					250					255		
Asn	Leu	Leu	Ser	Cys	Asp	Thr	His	His	Gln	Gln	Gly	Cys	Arg	Gly	Gly	

260 265 270  
 Arg Leu Asp Gly Ala Trp Trp Phe Leu Arg Arg Arg Gly Val Val Ser  
 275 280 285  
 Asp Asn Cys Tyr Pro Phe Ser Gly Arg Glu Gln Asn Glu Ala Ser Pro  
 290 295 300  
 Thr Pro Arg Cys Met Met His Ser Arg Ala Met Gly Arg Gly Lys Arg  
 305 310 315 320  
 Gln Ala Thr Ser Arg Cys Pro Asn Gly Gln Val Asp Ser Asn Asp Ile  
 325 330 335  
 Tyr Gln Val Thr Pro Ala Tyr Arg Leu Gly Ser Asp Glu Lys Glu Ile  
 340 345 350  
 Met Lys Glu Leu Met Glu Asn Gly Pro Val Gln Ala Leu Met Glu Val  
 355 360 365  
 His Glu Asp Phe Phe Leu Tyr Gln Arg Gly Ile Tyr Ser His Thr Pro  
 370 375 380  
 Val Ser Gln Gly Arg Pro Glu Gln Tyr Arg Arg His Gly Thr His Ser  
 385 390 395 400  
 Val Lys Ile Thr Gly Trp Gly Glu Glu Thr Leu Pro Asp Gly Arg Thr  
 405 410 415  
 Ile Lys Tyr Trp Thr Ala Ala Asn Ser Trp Gly Pro Trp Trp Gly Glu  
 420 425 430  
 Arg Gly His Phe Arg Ile Val Arg Gly Thr Asn Glu Cys Asp Ile Glu  
 435 440 445  
 Thr Phe Val Leu Gly Val Trp Gly Arg Val Gly Met Glu Asp Met Gly  
 450 455 460  
 His His  
 465

<210> 45  
 <211> 422  
 <212> PRT  
 <213> Mouse

<400> 45  
 Met Asp Phe Trp Leu Trp Leu Leu Tyr Phe Leu Pro Val Ser Gly Ala  
 1 5 10 15  
 Leu Arg Val Leu Pro Glu Val Gln Leu Asn Val Glu Trp Gly Gly Ser  
 20 25 30  
 Ile Ile Ile Glu Cys Pro Leu Pro Gln Leu His Val Arg Met Tyr Leu  
 35 40 45  
 Cys Arg Gln Met Ala Lys Pro Gly Ile Cys Ser Thr Val Val Ser Asn  
 50 55 60  
 Thr Phe Val Lys Lys Glu Tyr Glu Arg Arg Val Thr Leu Thr Pro Cys  
 65 70 75 80  
 Leu Asp Lys Lys Leu Phe Leu Val Glu Met Thr Gln Leu Thr Glu Asn  
 85 90 95  
 Asp Asp Gly Ile Tyr Ala Cys Gly Val Gly Met Lys Thr Asp Lys Gly  
 100 105 110  
 Lys Thr Gln Lys Ile Thr Leu Asn Val His Asn Glu Tyr Pro Glu Pro  
 115 120 125  
 Phe Trp Glu Asp Glu Trp Thr Ser Glu Arg Pro Arg Trp Leu His Arg  
 130 135 140  
 Phe Leu Gln His Gln Met Pro Trp Leu His Gly Ser Glu His Pro Ser  
 145 150 155 160  
 Ser Ser Gly Val Ile Ala Lys Val Thr Thr Pro Ala Ser Lys Thr Glu  
 165 170 175  
 Ala Pro Pro Val His Gln Pro Ser Ser Ile Thr Ser Val Thr Gln His

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      180      185      190
Pro Arg Val Tyr Arg Ala Phe Ser Val Ser Ala Thr Lys Ser Pro Ala
195      200      205
Leu Leu Pro Ala Thr Thr Ala Ser Lys Thr Ser Thr Gln Gln Ala Ile
210      215      220
Arg Pro Leu Glu Ala Ser Tyr Ser His His Thr Arg Leu His Glu Gln
225      230      235      240
Arg Thr Arg His His Gly Pro His Tyr Gly Arg Glu Asp Arg Gly Leu
245      250      255
His Ile Pro Ile Pro Glu Phe His Ile Leu Ile Pro Thr Phe Leu Gly
260      265      270
Phe Leu Leu Leu Val Leu Leu Gly Leu Val Val Lys Arg Ala Ile Gln
275      280      285
Arg Arg Arg Ala Ser Ser Arg Arg Ala Gly Arg Leu Ala Met Arg Arg
290      295      300
Arg Gly Arg Gly Ala Ser Arg Pro Phe Pro Thr Gln Arg Arg Asp Ala
305      310      315      320
Pro Gln Arg Pro Arg Ser Gln Asn Asn Val Tyr Ser Ala Cys Pro Arg
325      330      335
Arg Ala Arg Gly Pro Asp Ser Leu Gly Pro Ala Glu Ala Pro Leu Leu
340      345      350
Asn Ala Pro Ala Ser Ala Ser Pro Ala Ser Pro Gln Val Leu Glu Ala
355      360      365
Pro Trp Pro His Thr Pro Ser Leu Lys Met Ser Cys Glu Tyr Val Ser
370      375      380
Leu Gly Tyr Gln Pro Ala Val Asn Leu Glu Asp Pro Asp Ser Asp Asp
385      390      395      400
Tyr Ile Asn Ile Pro Asp Pro Ser His Leu Pro Ser Tyr Ala Pro Gly
405      410      415
Pro Arg Ser Ser Cys Gln
420

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<210> 46  
 <211> 228  
 <212> PRT  
 <213> Mouse

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<400> 46
Met Lys Ala Leu Arg Ala Val Leu Leu Ile Leu Leu Leu Ser Gly Gln
1      5      10      15
Pro Gly Ser Gly Trp Ala Gln Glu Asp Gly Asp Ala Asp Pro Glu Pro
20      25      30
Glu Asn Tyr Asn Tyr Asp Asp Asp Asp Glu Glu Glu Glu Glu Glu
35      40      45
Thr Asn Met Ile Pro Gly Ser Arg Asp Arg Ala Pro Leu Gln Cys Tyr
50      55      60
Phe Cys Gln Val Leu His Ser Gly Glu Ser Cys Asn Gln Thr Gln Ser
65      70      75      80
Cys Ser Ser Ser Lys Pro Phe Cys Ile Thr Leu Val Ser His Ser Gly
85      90      95
Thr Asp Lys Gly Tyr Leu Thr Thr Tyr Ser Met Trp Cys Thr Asp Thr
100      105      110
Cys Gln Pro Ile Ile Lys Thr Val Gly Gly Thr Gln Met Thr Gln Thr
115      120      125
Cys Cys Gln Ser Thr Leu Cys Asn Ile Pro Pro Trp Gln Asn Pro Gln
130      135      140
Val Gln Asn Pro Leu Gly Gly Arg Ala Asp Ser Pro Leu Glu Ser Gly

```

145					150					155				160
Thr	Arg	His	Pro	Gln	Gly	Gly	Lys	Phe	Ser	His	Pro	Gln	Val	Val
				165					170					175
Ala	Ala	His	Pro	Gln	Ser	Asp	Gly	Ala	Asn	Leu	Pro	Lys	Ser	Gly
			180					185					190	
Ala	Asn	Gln	Pro	Gln	Gly	Ser	Gly	Ala	Gly	Tyr	Pro	Ser	Gly	Trp
		195					200				205			
Lys	Phe	Gly	Asn	Ile	Ala	Leu	Leu	Leu	Ser	Phe	Phe	Thr	Cys	Leu
	210					215					220			
Ala	Ser	Gly	Ala											
225														

<210> 47  
 <211> 269  
 <212> PRT  
 <213> Mouse

<400> 47														
Gly	Cys	Ser	Asp	Gly	Glu	Asn	Gln	Arg	Ser	Gly	His	Leu	Ser	Val
1				5					10					15
Leu	Gln	Leu	Ser	Leu	Lys	Val	Leu	Leu	Ile	Arg	Met	Ala	Ser	Gly
			20					25					30	
Phe	Tyr	Leu	Ser	Cys	Met	Val	Leu	Gly	Ser	Leu	Gly	Ser	Met	Cys
		35					40					45		
Leu	Phe	Thr	Ala	Tyr	Trp	Met	Gln	Tyr	Trp	Arg	Gly	Gly	Phe	Ala
	50					55				60				
Asp	Gly	Thr	Val	Leu	Met	Phe	Asn	Trp	His	Pro	Val	Leu	Met	Val
65					70				75					80
Gly	Met	Val	Val	Leu	Tyr	Gly	Ala	Ala	Ser	Leu	Val	Tyr	Arg	Leu
			85						90					95
Ser	Ser	Trp	Val	Gly	Pro	Arg	Leu	Pro	Trp	Lys	Val	Leu	His	Ala
		100						105					110	
Leu	His	Leu	Leu	Ala	Phe	Thr	Cys	Thr	Val	Val	Gly	Leu	Ile	Ala
	115						120					125		
Phe	Arg	Phe	His	Asn	His	Ser	Arg	Ile	Ala	His	Leu	Tyr	Ser	Leu
	130					135					140			
Ser	Trp	Leu	Gly	Ile	Thr	Thr	Val	Val	Leu	Phe	Ala	Cys	Gln	Trp
145						150				155				160
Leu	Gly	Phe	Ala	Val	Phe	Leu	Leu	Pro	Trp	Ala	Ser	Gln	Trp	Leu
			165						170					175
Ser	Leu	Leu	Lys	Pro	Leu	His	Val	Phe	Phe	Gly	Ala	Cys	Ile	Leu
			180					185					190	
Leu	Ser	Ile	Thr	Ser	Val	Ile	Ser	Gly	Ile	Asn	Glu	Lys	Leu	Phe
	195						200					205		
Val	Leu	Lys	Asn	Ala	Thr	Lys	Pro	Tyr	Ser	Ser	Leu	Pro	Gly	Glu
	210					215					220			
Val	Phe	Ala	Asn	Ser	Thr	Gly	Leu	Leu	Val	Val	Ala	Phe	Gly	Leu
225						230				235				240
Val	Leu	Tyr	Val	Leu	Leu	Ala	Ser	Ser	Trp	Lys	Arg	Pro	Asp	Pro
			245						250					255
Ala	Leu	Thr	Asp	Arg	Gln	Pro	Leu	Leu	His	Asp	Arg	Glu		
			260					265						

<210> 48  
 <211> 188  
 <212> PRT  
 <213> Mouse

&lt;400&gt; 48

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Met Arg Leu Pro Leu Pro Leu Leu Leu Leu Phe Gly Cys Arg Ala Ile
 1           5           10           15
Leu Gly Ser Ala Gly Asp Arg Val Ser Leu Ser Ala Ser Ala Pro Thr
          20           25           30
Leu Asp Asp Glu Glu Lys Tyr Ser Ala His Met Pro Ala His Leu Arg
          35           40           45
Cys Asp Ala Cys Arg Ala Val Ala Phe Gln Met Gly Gln Arg Leu Ala
          50           55           60
Lys Ala Glu Ala Lys Ser His Thr Pro Asp Ala Ser Gly Leu Gln Glu
65           70           75           80
Leu Ser Glu Ser Thr Tyr Thr Asp Val Leu Asp Gln Thr Cys Ser Gln
          85           90           95
Asn Trp Gln Ser Tyr Gly Val His Glu Val Asn Gln Met Lys Arg Leu
          100          105          110
Thr Gly Pro Gly Leu Ser Lys Gly Pro Glu Pro Arg Ile Ser Val Met
          115          120          125
Ile Ser Gly Gly Pro Trp Pro Asn Arg Leu Ser Lys Thr Cys Phe His
          130          135          140
Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala Tyr Arg Gln
145          150          155          160
Gly Gln Ala Asn Leu Glu Ala Leu Leu Cys Gly Gly Thr His Gly Pro
          165          170          175
Cys Ser Gln Glu Ile Leu Ala Gln Arg Glu Glu Leu
          180          185

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&lt;210&gt; 49

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 49

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Met Ile Pro Gln Val Val Thr Ser Glu Thr Val Thr Val Ile Ser Pro
 1           5           10           15
Asn Gly Ile Ser Phe Pro Gln Thr Asp Lys Pro Gln Pro Ser His Gln
          20           25           30
Ser Gln Asp Arg Leu Lys Lys His Leu Lys Ala Glu Ile Lys Val Met
          35           40           45
Ala Ala Ile Gln Ile Met Cys Ala Val Met Val Leu Ser Leu Gly Ile
          50           55           60
Ile Leu Ala Ser Val Pro Ser Asn Leu His Phe Thr Ser Val Phe Ser
65           70           75           80
Ile Leu Leu Glu Ser Gly Tyr Pro Phe Val Gly Ala Leu Phe Phe Ala
          85           90           95
Ile Ser Gly Ile Leu Ser Ile Val Thr Glu Lys Lys Met Thr Lys Pro
          100          105          110
Leu Val His Ser Ser Leu Ala Leu Ser Ile Leu Ser Val Leu Ser Ala
          115          120          125
Leu Thr Gly Ile Ala Ile Leu Ser Val Ser Leu Ala Ala Leu Glu Pro
          130          135          140
Ala Leu Gln Gln Cys Lys Leu Ala Phe Thr Gln Leu Asp Thr Thr Gln
145          150          155          160
Asp Ala Tyr His Phe Phe Ser Pro Glu Pro Leu Asn Ser Cys Phe Val
          165          170          175
Ala Lys Ala Ala Leu Thr Gly Val Phe Ser Leu Met Leu Ile Ser Ser
          180          185          190

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Val Leu Glu Leu Gly Leu Ala Val Leu Thr Ala Thr Leu Trp Trp Lys  
 195 200 205  
 Gln Ser Ser Ser Ala Phe Ser Gly Asn Val Ile Phe Leu Ser Gln Asn  
 210 215 220  
 Ser Lys Asn Lys Ser Ser Val Ser Ser Glu Ser Leu Cys Asn Pro Thr  
 225 230 235 240  
 Tyr Glu Asn Ile Leu Thr Ser  
 245

<210> 50  
 <211> 182  
 <212> PRT  
 <213> Mouse

<400> 50  
 Pro Phe His Cys His Val Trp Ser Leu Cys Leu Gln Gly Ser Lys Gln  
 1 5 10 15  
 Ser Gly Leu Cys Gln Val Gln Arg Asp Leu Gly Arg Asp Asp Arg Ser  
 20 25 30  
 Val Arg Gly Ser Lys Ala Ala Val Ala Gly Ala Val Val Gly Thr  
 35 40 45  
 Phe Val Gly Leu Val Leu Ile Ala Gly Leu Val Leu Leu Tyr Gln Arg  
 50 55 60  
 Arg Ser Lys Thr Leu Glu Glu Leu Ala Asn Asp Ile Lys Glu Asp Ala  
 65 70 75 80  
 Ile Ala Pro Arg Thr Leu Pro Trp Thr Lys Gly Ser Asp Thr Ile Ser  
 85 90 95  
 Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg Pro  
 100 105 110  
 Pro Lys Ala Ala Pro Pro Arg Pro Gly Thr Phe Thr Pro Thr Pro Ser  
 115 120 125  
 Val Ser Ser Gln Ala Leu Ser Ser Pro Arg Leu Pro Arg Val Asp Glu  
 130 135 140  
 Pro Pro Pro Gln Ala Val Ser Leu Thr Pro Gly Gly Val Ser Ser Ser  
 145 150 155 160  
 Ala Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
 165 170 175  
 Gln Ala Gly Ser Leu Val  
 180

<210> 51  
 <211> 248  
 <212> PRT  
 <213> Mouse

<400> 51  
 Met Ser Trp Ser Pro Ile Leu Pro Phe Leu Ser Leu Leu Leu Leu Leu  
 1 5 10 15  
 Phe Pro Leu Glu Val Pro Arg Ala Ala Thr Ala Ser Leu Ser Gln Ala  
 20 25 30  
 Ser Ser Glu Gly Thr Thr Thr Cys Lys Val His Asp Val Cys Leu Leu  
 35 40 45  
 Gly Pro Arg Pro Leu Pro Pro Ser Pro Pro Val Arg Val Ser Leu Tyr  
 50 55 60  
 Tyr Glu Ser Leu Cys Gly Ala Cys Arg Tyr Phe Leu Val Arg Asp Leu  
 65 70 75 80  
 Phe Pro Thr Trp Leu Met Val Met Glu Ile Met Asn Ile Thr Leu Val

Pro	Tyr	Gly	Asn	85	Gln	Glu	Arg	Asn	90	Val	Ser	Gly	Thr	Trp	95	Glu	Phe
			100	Ala				105						110			
Thr	Cys	Gln	His	Gly	Glu	Leu	Glu	Cys	Arg	Leu	Asn	Met	Val	Glu	Ala		
		115					120						125				
Cys	Leu	Leu	Asp	Lys	Leu	Glu	Lys	Glu	Ala	Ala	Phe	Leu	Thr	Ile	Val		
		130				135						140					
Cys	Met	Glu	Glu	Met	Asp	Asp	Met	Glu	Lys	Lys	Leu	Gly	Pro	Cys	Leu		
145				150						155					160		
Gln	Val	Tyr	Ala	Pro	Glu	Val	Ser	Pro	Glu	Ser	Ile	Met	Glu	Cys	Ala		
			165					170						175			
Thr	Gly	Lys	Arg	Gly	Thr	Gln	Leu	Met	His	Glu	Asn	Ala	Gln	Leu	Thr		
		180						185					190				
Asp	Ala	Leu	His	Pro	Pro	His	Glu	Tyr	Val	Pro	Trp	Val	Leu	Val	Asn		
		195					200					205					
Glu	Lys	Pro	Leu	Lys	Asp	Pro	Ser	Glu	Leu	Leu	Ser	Ile	Val	Cys	Gln		
		210				215					220						
Leu	Asp	Gln	Gly	Thr	Glu	Lys	Pro	Asp	Ile	Cys	Ser	Ser	Ile	Ala	Asp		
225					230					235					240		
Ser	Pro	Arg	Lys	Val	Cys	Tyr	Lys										
				245													

&lt;210&gt; 52

&lt;211&gt; 278

&lt;212&gt; PRT

&lt;213&gt; Mouse

&lt;400&gt; 52

Met	Gln	Thr	Met	Trp	Gly	Ser	Gly	Glu	Leu	Leu	Val	Ala	Trp	Phe	Leu		
1			5					10						15			
Val	Leu	Ala	Ala	Asp	Gly	Thr	Thr	Glu	His	Val	Tyr	Arg	Pro	Ser	Arg		
		20						25					30				
Arg	Val	Cys	Thr	Val	Gly	Ile	Ser	Gly	Gly	Ser	Ile	Ser	Glu	Thr	Phe		
		35				40						45					
Val	Gln	Arg	Val	Tyr	Gln	Pro	Tyr	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg		
	50				55						60						
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	Ser		
65				70					75						80		
Pro	Gly	Val	Thr	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	Gly	Trp		
			85					90						95			
Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	Ile	Cys	Gln		
		100						105					110				
Pro	Pro	Cys	Gly	Asn	Gly	Gly	Ser	Cys	Ile	Arg	Pro	Gly	His	Cys	Arg		
		115				120						125					
Cys	Pro	Val	Gly	Trp	Gln	Gly	Asp	Thr	Cys	Gln	Thr	Asp	Val	Asp	Glu		
		130				135					140						
Cys	Ser	Thr	Gly	Glu	Ala	Ser	Cys	Pro	Gln	Arg	Cys	Val	Asn	Thr	Val		
145				150						155					160		
Gly	Ser	Tyr	Trp	Cys	Gln	Gly	Trp	Glu	Gly	Gln	Ser	Pro	Ser	Ala	Asp		
			165					170						175			
Gly	Thr	Arg	Cys	Leu	Ser	Lys	Glu	Gly	Pro	Ser	Pro	Val	Ala	Pro	Asn		
		180						185					190				
Pro	Thr	Ala	Gly	Val	Asp	Ser	Met	Ala	Arg	Glu	Glu	Val	Tyr	Arg	Leu		
		195					200					205					
Gln	Ala	Arg	Val	Asp	Val	Leu	Glu	Gln	Lys	Leu	Gln	Leu	Val	Leu	Ala		
	210					215					220						
Pro	Leu	His	Ser	Leu	Ala	Ser	Arg	Ser	Thr	Glu	His	Gly	Leu	Gln	Asp		

```
<210> 53
<211> 409
<212> PRT
<213> Mouse
```

<400>	53														
Met	Lys	Leu	Lys	Gln	Arg	Val	Val	Leu	Leu	Ala	Ile	Leu	Leu	Val	Ile
1				5					10					15	
Phe	Ile	Phe	Thr	Lys	Val	Phe	Leu	Ile	Asp	Asn	Leu	Asp	Thr	Ser	Ala
			20					25					30		
Ala	Asn	Arg	Glu	Asp	Gln	Arg	Ala	Phe	His	Arg	Met	Met	Thr	Gly	Leu
		35					40					45			
Arg	Val	Glu	Leu	Val	Pro	Lys	Leu	Asp	His	Thr	Leu	Gln	Ser	Pro	Trp
	50					55					60				
Glu	Ile	Ala	Ala	Gln	Trp	Val	Val	Pro	Arg	Glu	Val	Tyr	Pro	Glu	Glu
65				70						75				80	
Thr	Pro	Glu	Leu	Gly	Ala	Ile	Met	His	Ala	Met	Ala	Thr	Lys	Lys	Ile
				85					90					95	
Ile	Lys	Ala	Asp	Val	Gly	Tyr	Lys	Gly	Thr	Gln	Leu	Lys	Ala	Leu	Leu
			100					105					110		
Ile	Leu	Glu	Gly	Gly	Gln	Lys	Val	Val	Phe	Lys	Pro	Lys	Arg	Tyr	Ser
		115					120					125			
Arg	Asp	Tyr	Val	Val	Glu	Gly	Glu	Pro	Tyr	Ala	Gly	Tyr	Asp	Arg	His
	130					135					140				
Asn	Ala	Glu	Val	Ala	Ala	Phe	His	Leu	Asp	Arg	Ile	Leu	Gly	Phe	Arg
145					150					155					160
Arg	Ala	Pro	Leu	Val	Val	Gly	Arg	Tyr	Val	Asn	Leu	Arg	Thr	Glu	Val
				165					170					175	
Lys	Pro	Val	Ala	Thr	Glu	Gln	Leu	Leu	Ser	Thr	Phe	Leu	Thr	Val	Gly
			180					185					190		
Asn	Asn	Thr	Cys	Phe	Tyr	Gly	Lys	Cys	Tyr	Tyr	Cys	Arg	Glu	Thr	Glu
		195					200					205			
Pro	Ala	Cys	Ala	Asp	Gly	Asp	Met	Met	Glu	Gly	Ser	Val	Thr	Leu	Trp
		210				215					220				
Leu	Pro	Asp	Val	Trp	Pro	Leu	Gln	Lys	His	Arg	His	Pro	Trp	Gly	Arg
225					230					235					240
Thr	Tyr	Arg	Glu	Gly	Lys	Leu	Ala	Arg	Trp	Glu	Tyr	Asp	Glu	Ser	Tyr
				245					250					255	
Cys	Asp	Ala	Val	Lys	Lys	Thr	Ser	Pro	Tyr	Asp	Ser	Gly	Pro	Arg	Leu
			260					265					270		
Leu	Asp	Ile	Ile	Asp	Thr	Ala	Val	Phe	Asp	Tyr	Leu	Ile	Gly	Asn	Ala
		275					280					285			
Asp	Arg	His	His	Tyr	Glu	Ser	Phe	Gln	Asp	Asp	Glu	Gly	Ala	Ser	Met
		290				295					300				
Leu	Ile	Leu	Leu	Asp	Asn	Ala	Lys	Ser	Phe	Gly	Asn	Pro	Ser	Leu	Asp
305					310					315					320
Glu	Arg	Ser	Ile	Leu	Ala	Pro	Leu	Tyr	Gln	Cys	Cys	Ile	Ile	Arg	Val
				325					330					335	
Ser	Thr	Trp	Asn	Arg	Leu	Asn	Tyr	Leu	Lys	Asn	Gly	Val	Leu	Lys	Ser



```
<210> 54
<211> 697
<212> PRT
<213> Mouse
```

<400>	54														
Met	Arg	Leu	Thr	Val	Gly	Ala	Leu	Leu	Ala	Cys	Ala	Ala	Leu	Gly	Leu
1				5					10				15		
Cys	Leu	Ala	Val	Pro	Asp	Lys	Thr	Val	Lys	Trp	Cys	Ala	Val	Ser	Glu
			20					25					30		
His	Glu	Asn	Thr	Lys	Cys	Ile	Ser	Phe	Arg	Asp	His	Met	Lys	Thr	Val
		35					40				45				
Leu	Pro	Pro	Asp	Gly	Pro	Arg	Leu	Ala	Cys	Val	Lys	Lys	Thr	Ser	Tyr
	50					55				60					
Pro	Asp	Cys	Ile	Lys	Ala	Ile	Ser	Ala	Ser	Glu	Ala	Asp	Ala	Met	Thr
65					70					75					80
Leu	Asp	Gly	Gly	Trp	Val	Tyr	Asp	Ala	Gly	Leu	Thr	Pro	Asn	Asn	Leu
				85					90					95	
Lys	Pro	Val	Ala	Glu	Phe	Tyr	Gly	Ser	Val	Glu	His	Pro	Gln	Thr	
			100				105					110			
Tyr	Tyr	Tyr	Ala	Val	Ala	Val	Val	Lys	Lys	Gly	Thr	Asp	Phe	Gln	Leu
		115					120					125			
Asn	Gln	Leu	Glu	Gly	Lys	Lys	Ser	Cys	His	Thr	Gly	Leu	Gly	Arg	Ser
	130					135					140				
Ala	Gly	Trp	Val	Ile	Pro	Ile	Gly	Leu	Leu	Phe	Cys	Lys	Leu	Ser	Glu
145					150					155					160
Pro	Arg	Ser	Pro	Leu	Glu	Lys	Ala	Val	Ser	Phe	Phe	Ser	Gly	Ser	
				165					170					175	
Cys	Val	Pro	Cys	Ala	Asp	Pro	Val	Ala	Phe	Pro	Lys	Leu	Cys	Gln	Leu
			180					185					190		
Cys	Pro	Gly	Cys	Gly	Cys	Ser	Ser	Thr	Gln	Pro	Phe	Phe	Gly	Tyr	Val
		195					200					205			
Gly	Ala	Phe	Lys	Cys	Leu	Lys	Asp	Gly	Gly	Gly	Asp	Val	Ala	Phe	Val
	210					215					220				
Lys	His	Thr	Thr	Ile	Phe	Glu	Val	Leu	Pro	Glu	Lys	Ala	Asp	Arg	Asp
225					230					235					240
Gln	Tyr	Glu	Leu	Leu	Cys	Leu	Asp	Asn	Thr	Arg	Lys	Pro	Val	Asp	Gln
				245					250					255	
Tyr	Glu	Asp	Cys	Tyr	Leu	Ala	Arg	Ile	Pro	Ser	His	Ala	Val	Val	Ala
			260					265					270		
Arg	Lys	Asn	Asn	Gly	Lys	Glu	Asp	Leu	Ile	Trp	Glu	Ile	Leu	Lys	Val
		275					280					285			
Ala	Gln	Glu	His	Phe	Gly	Lys	Gly	Lys	Ser	Lys	Asp	Phe	Gln	Leu	Phe
	290					295					300				
Ser	Ser	Pro	Leu	Gly	Lys	Asp	Leu	Leu	Phe	Lys	Asp	Ser	Ala	Phe	Gly
305					310					315					320
Leu	Leu	Arg	Val	Pro	Pro	Arg	Met	Asp	Tyr	Arg	Leu	Tyr	Leu	Gly	His

```
<210> 55
<211> 400
<212> PRT
<213> Mouse
```

Gly Ala Pro Thr Pro Ala Tyr Val Arg Ser Ala Arg Arg Thr Glu Pro  
1 5 10 15  
Leu Ala Ser Gly Ala Arg Ser Arg Leu Cys Gln Cys Arg Arg Val Pro

```
<210> 56
<211> 174
<212> PRT
<213> Mouse
```

<400> 56  
Met Pro Ala Cys Arg Leu Cys Leu Leu Ala Ala Gly Leu Leu Leu Gly  
1 5 10 15  
Leu Leu Leu Phe Thr Pro Ile Ser Ala Thr Gly Thr Asp Ala Glu Lys

```

                20                25                30
Pro Gly Glu Cys Pro Gln Leu Glu Pro Ile Thr Asp Cys Val Leu Glu
   35                40                45
Cys Thr Leu Asp Lys Asp Cys Ala Asp Asn Arg Lys Cys Cys Gln Ala
   50                55                60
Gly Cys Ser Ser Val Cys Ser Lys Pro Asn Gly Pro Ser Glu Gly Glu
   65                70                75
Leu Ser Gly Thr Asp Thr Lys Leu Ser Glu Thr Gly Thr Thr Thr Gln
   85                90                95
Ser Ala Gly Leu Asp His Thr Thr Lys Pro Pro Gly Gly Gln Val Ser
  100                105                110
Thr Lys Pro Pro Ala Val Thr Arg Glu Gly Leu Gly Val Arg Glu Lys
  115                120                125
Gln Gly Thr Cys Pro Ser Val Asp Ile Pro Lys Leu Gly Leu Cys Glu
  130                135                140
Asp Gln Cys Gln Val Asp Ser Gln Cys Ser Gly Asn Met Lys Cys Cys
  145                150                155
Arg Asn Gly Cys Gly Lys Met Ala Cys Thr Thr Pro Lys Phe
                165                170

```

<210> 57  
 <211> 173  
 <212> PRT  
 <213> Mouse

```

<400> 57
Val Arg Asn Gly Asp Leu Phe Phe Lys Lys Val Gln Val Glu Asp Gly
  1      5      10      15
Gly Val Tyr Thr Cys Tyr Ala Met Gly Glu Thr Phe Asn Glu Thr Leu
  20      25      30
Ser Val Glu Leu Lys Val Tyr Asn Phe Thr Leu His Gly His His Asp
  35      40      45
Thr Leu Asn Thr Ala Tyr Thr Thr Leu Val Gly Cys Ile Leu Ser Val
  50      55      60
Val Leu Val Leu Ile Tyr Leu Tyr Leu Thr Pro Cys Arg Cys Trp Cys
  65      70      75      80
Arg Gly Val Glu Lys Pro Ser Ser His Gln Gly Asp Ser Leu Ser Ser
  85      90      95
Ser Met Leu Ser Thr Thr Pro Asn His Asp Pro Met Ala Gly Gly Asp
  100     105     110
Lys Asp Asp Gly Phe Asp Arg Arg Val Ala Phe Leu Glu Pro Ala Gly
  115     120     125
Pro Gly Gln Gly Gln Asn Gly Lys Leu Lys Pro Gly Asn Thr Leu Pro
  130     135     140
Val Pro Glu Ala Thr Gly Lys Gly Gln Arg Arg Met Ser Asp Pro Glu
  145     150     155     160
Ser Val Ser Ser Val Phe Ser Asp Thr Pro Ile Val Val
                165                170

```

<210> 58  
 <211> 88  
 <212> PRT  
 <213> Mouse

```

<400> 58
Met Glu Glu Ile Thr Cys Ala Phe Leu Leu Leu Leu Ala Gly Leu Pro
  1      5      10      15

```

Ala Leu Glu Ala Ser Asp Pro Val Asp Lys Asp Ser Pro Phe Tyr Tyr  
 20 25 30  
 Asp Trp Glu Ser Leu Gln Leu Gly Gly Leu Ile Phe Gly Gly Leu Leu  
 35 40 45  
 Cys Ile Ala Gly Ile Ala Met Ala Leu Ser Gly Lys Cys Lys Cys Arg  
 50 55 60  
 Arg Thr His Lys Pro Ser Ser Leu Pro Gly Lys Ala Thr Pro Leu Ile  
 65 70 75 80  
 Ile Pro Gly Ser Ala Asn Thr Cys  
 85

<210> 59  
 <211> 171  
 <212> PRT  
 <213> Mouse

<400> 59  
 Leu Ser Val Val Leu Gly Gly Thr Leu Tyr Ile Gly His Tyr Leu Ala  
 1 5 10 15  
 Met Tyr Ser Glu Gly Ala Pro Phe Trp Thr Gly Ile Val Ala Met Leu  
 20 25 30  
 Ala Gly Ala Val Ala Phe Leu His Lys Lys Arg Gly Gly Thr Cys Trp  
 35 40 45  
 Ala Leu Met Arg Thr Leu Leu Val Leu Ala Ser Phe Cys Thr Ala Val  
 50 55 60  
 Ala Ala Ile Val Ile Gly Ser Arg Glu Leu Asn Tyr Tyr Trp Tyr Phe  
 65 70 75 80  
 Leu Gly Asp Asp Val Cys Gln Arg Asp Ser Ser Tyr Gly Trp Ser Thr  
 85 90 95  
 Met Pro Arg Thr Thr Pro Val Pro Glu Glu Ala Asp Arg Ile Ala Leu  
 100 105 110  
 Cys Ile Tyr Tyr Thr Ser Met Leu Lys Thr Leu Leu Met Ser Leu Gln  
 115 120 125  
 Ala Met Leu Leu Gly Ile Trp Val Leu Leu Leu Leu Ala Ser Leu Thr  
 130 135 140  
 Pro Val Cys Val Tyr Ile Trp Lys Arg Phe Phe Thr Lys Ala Glu Thr  
 145 150 155 160  
 Glu Glu Lys Lys Leu Leu Gly Ala Ala Val Ile  
 165 170

<210> 60  
 <211> 318  
 <212> PRT  
 <213> Mouse

<400> 60  
 Met Leu Gln His Thr Ser Leu Val Leu Leu Leu Ala Ser Ile Trp Thr  
 1 5 10 15  
 Thr Arg His Pro Val Gln Gly Ala Asp Leu Val Gln Asp Leu Ser Ile  
 20 25 30  
 Ser Thr Cys Arg Ile Met Gly Val Ala Leu Val Gly Arg Asn Lys Asn  
 35 40 45  
 Pro Gln Met Asn Phe Thr Glu Ala Asn Glu Ala Cys Lys Met Leu Gly  
 50 55 60  
 Leu Thr Leu Ala Ser Arg Asp Gln Val Glu Ser Ala Gln Lys Ser Gly  
 65 70 75 80  
 Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Glu Gln Phe Ser Val Ile

85						90						95					
Pro	Arg	Ile	Phe	Ser	Asn	Pro	Arg	Cys	Gly	Lys	Asn	Gly	Lys	Gly	Val		
			100				105						110				
Leu	Ile	Trp	Asn	Ala	Pro	Ser	Ser	Gln	Lys	Phe	Lys	Ala	Tyr	Cys	His		
			115				120						125				
Asn	Ser	Ser	Asp	Thr	Trp	Val	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Val	Thr		
			130				135						140				
Thr	Phe	Tyr	Pro	Val	Leu	Asp	Thr	Gln	Thr	Pro	Ala	Thr	Glu	Phe	Ser		
145				150						155			160				
Val	Ser	Ser	Ser	Ala	Tyr	Leu	Ala	Ser	Ser	Pro	Asp	Ser	Thr	Thr	Pro		
			165						170			175					
Val	Ser	Ala	Thr	Thr	Arg	Ala	Pro	Pro	Leu	Thr	Ser	Met	Ala	Arg	Lys		
			180			185						190					
Thr	Lys	Lys	Ile	Cys	Ile	Thr	Glu	Val	Tyr	Thr	Glu	Pro	Ile	Thr	Met		
			195			200						205					
Ala	Thr	Glu	Thr	Glu	Ala	Phe	Val	Ala	Ser	Gly	Ala	Ala	Phe	Lys	Asn		
			210			215						220					
Glu	Ala	Ala	Gly	Phe	Gly	Gly	Val	Pro	Thr	Ala	Leu	Leu	Val	Leu	Ala		
225				230						235			240				
Leu	Leu	Phe	Phe	Gly	Ala	Ala	Ala	Val	Leu	Ala	Val	Cys	Tyr	Val	Lys		
			245			250						255					
Arg	Tyr	Val	Lys	Ala	Phe	Pro	Phe	Thr	Thr	Lys	Asn	Gln	Gln	Lys	Glu		
			260			265						270					
Met	Ile	Glu	Thr	Lys	Val	Val	Lys	Glu	Glu	Lys	Ala	Asp	Asp	Val	Asn		
			275			280						285					
Ala	Asn	Glu	Glu	Ser	Lys	Lys	Thr	Ile	Lys	Asn	Pro	Glu	Glu	Ala	Lys		
			290			295						300					
Ser	Pro	Pro	Lys	Thr	Thr	Val	Arg	Cys	Leu	Glu	Ala	Glu	Val				
305				310						315							

```
<210> 61
<211> 93
<212> PRT
<213> Mouse
```

```

<400> 61
Ala His Met Val Trp Ala Asn Leu Ala Val Phe Val Ile Cys Phe Leu
 1          5          10          15
Pro Leu His Val Leu Thr Val Gln Val Ser Leu Asn Leu Asn Thr
 20          25          30
Cys Ala Ala Arg Asp Thr Phe Ser Arg Ala Leu Ser Ile Thr Gly Lys
 35          40          45
Leu Ser Asp Thr Asn Cys Cys Leu Asp Ala Ile Cys Tyr Tyr Tyr Met
 50          55          60
Ala Arg Glu Phe Gln Glu Ala Ser Lys Pro Ala Thr Ser Ser Asn Thr
 65          70          75          80
Pro His Lys Ser Gln Asp Ser Gln Ile Leu Ser Leu Thr
 85          90

```

```
<210> 62
<211> 408
<212> PRT
<213> Mouse
```

```
<400> 62
Met Ala Gln Leu Ala Arg Ala Thr Arg Ser Pro Leu Ser Trp Leu Leu
  1             5             10             15
```

Leu Leu Phe Cys Tyr Ala Leu Arg Lys Ala Gly Gly Asp Ile Arg Val  
 20 25 30  
 Leu Val Pro Tyr Asn Ser Thr Gly Val Leu Gly Gly Ser Thr Thr Leu  
 35 40 45  
 His Cys Ser Leu Thr Ser Asn Glu Asn Val Thr Ile Thr Gln Ile Thr  
 50 55 60  
 Trp Met Lys Lys Asp Ser Gly Gly Ser His Ala Leu Val Ala Val Phe  
 65 70 75 80  
 His Pro Lys Lys Gly Pro Asn Ile Lys Glu Pro Glu Arg Val Lys Phe  
 85 90 95  
 Leu Ala Ala Gln Gln Asp Leu Arg Asn Ala Ser Leu Ala Ile Ser Asn  
 100 105 110  
 Leu Ser Val Glu Asp Glu Gly Ile Tyr Glu Cys Gln Ile Ala Thr Phe  
 115 120 125  
 Pro Arg Gly Ser Arg Ser Thr Asn Ala Trp Leu Lys Val Gln Ala Arg  
 130 135 140  
 Pro Lys Asn Thr Ala Glu Ala Leu Glu Pro Ser Pro Thr Leu Ile Leu  
 145 150 155 160  
 Gln Asp Val Ala Lys Cys Ile Ser Ala Asn Gly His Pro Pro Gly Arg  
 165 170 175  
 Ile Ser Trp Pro Ser Asn Val Asn Gly Ser His Arg Glu Met Lys Glu  
 180 185 190  
 Pro Gly Ser Gln Pro Gly Thr Thr Thr Val Thr Ser Tyr Leu Ser Met  
 195 200 205  
 Val Pro Ser Arg Gln Ala Asp Gly Lys Asn Ile Thr Cys Thr Val Glu  
 210 215 220  
 His Glu Ser Leu Gln Glu Leu Asp Gln Leu Leu Val Thr Leu Ser Gln  
 225 230 235 240  
 Pro Tyr Pro Pro Glu Asn Val Ser Ile Ser Gly Tyr Asp Gly Asn Trp  
 245 250 255  
 Tyr Val Gly Leu Thr Asn Leu Thr Leu Thr Cys Glu Ala His Ser Lys  
 260 265 270  
 Pro Ala Pro Asp Met Ala Gly Tyr Asn Trp Ser Thr Asn Thr Gly Asp  
 275 280 285  
 Phe Pro Asn Ser Val Lys Arg Gln Gly Asn Met Leu Leu Ile Ser Thr  
 290 295 300  
 Val Glu Asp Gly Leu Asn Asn Thr Val Ile Val Cys Glu Val Thr Asn  
 305 310 315 320  
 Ala Leu Gly Ser Gly Gln Gly Gln Val His Ile Ile Val Lys Glu Lys  
 325 330 335  
 Pro Glu Asn Met Gln Gln Asn Thr Arg Leu His Leu Gly Tyr Ile Phe  
 340 345 350  
 Leu Ile Val Phe Val Leu Ala Val Val Ile Ile Ile Ala Ala Leu Tyr  
 355 360 365  
 Thr Ile Arg Arg Cys Arg His Gly Arg Ala Leu Gln Ser Asn Pro Ser  
 370 375 380  
 Glu Arg Glu Asn Val Gln Tyr Ser Ser Val Asn Gly Asp Cys Arg Leu  
 385 390 395 400  
 Asn Met Glu Pro Asn Ser Thr Arg  
 405

<210> 63  
 <211> 278  
 <212> PRT  
 <213> Mouse

<400> 63

```

Met Phe Leu Val Gly Ser Leu Val Val Leu Cys Gly Leu Leu Ala His
 1      5      10      15
Ser Thr Ala Gln Leu Ala Gly Leu Pro Leu Pro Leu Gly Gln Gly Pro
 20      25      30
Pro Leu Pro Leu Asn Gln Gly Pro Pro Leu Pro Leu Asn Gln Gly Gln
 35      40      45
Leu Leu Pro Leu Ala Gln Gly Leu Pro Leu Ala Val Ser Pro Ala Leu
 50      55      60
Pro Ser Asn Pro Thr Asp Leu Leu Ala Gly Lys Phe Thr Asp Ala Leu
 65      70      75      80
Ser Gly Gly Leu Leu Ser Gly Gly Leu Leu Gly Ile Leu Glu Asn Ile
 85      90      95
Pro Leu Leu Asp Val Ile Lys Ser Gly Gly Gly Asn Ser Asn Gly Leu
 100     105     110
Val Gly Gly Leu Leu Gly Lys Leu Thr Ser Ser Val Pro Leu Leu Asn
 115     120     125
Asn Ile Leu Asp Ile Lys Ile Thr Asp Pro Gln Leu Leu Glu Leu Gly
 130     135     140
Leu Val Gln Ser Pro Asp Gly His Arg Leu Tyr Val Thr Ile Pro Leu
 145     150     155     160
Gly Leu Thr Leu Asn Val Asn Met Pro Val Val Gly Ser Leu Leu Gln
 165     170     175
Leu Ala Val Lys Leu Asn Ile Thr Ala Glu Val Leu Ala Val Lys Asp
 180     185     190
Asn Gln Gly Arg Ile His Leu Val Leu Gly Asp Cys Thr His Ser Pro
 195     200     205
Gly Ser Leu Lys Ile Ser Leu Asn Gly Val Thr Pro Val Gln Ser
 210     215     220
Phe Leu Asp Asn Leu Thr Gly Ile Leu Thr Lys Val Leu Pro Glu Leu
 225     230     235     240
Ile Gln Gly Lys Val Cys Pro Leu Val Asn Gly Ile Leu Ser Gly Leu
 245     250     255
Asp Val Thr Leu Val His Asn Ile Ala Glu Leu Leu Ile His Gly Leu
 260     265     270
Gln Phe Val Ile Lys Val
 275

```

<210> 64  
 <211> 264  
 <212> PRT  
 <213> Mouse

```

<400> 64
Met Ala Thr Thr Thr Cys Gln Val Val Gly Leu Leu Leu Ser Leu Leu
 1      5      10      15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20      25      30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ala Val Phe Gln His Glu Gly
 35      40      45
Leu Trp Arg Ser Cys Val Gln Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50      55      60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
 65      70      75      80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Val Ile Gly Ile Leu Val
 85      90      95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Asp Asp Ser
 100     105     110

```



Ala Lys Ala Lys Met Thr Leu Thr Ser Gly Ile Leu Phe Ile Ile Ser  
 115 120 125  
 Gly Ile Cys Ala Ile Ile Gly Val Ser Val Phe Ala Asn Met Leu Val  
 130 135 140  
 Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Ser Gly Met Gly Gly  
 145 150 155 160  
 Met Gly Gly Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala  
 165 170 175  
 Ala Leu Phe Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly  
 180 185 190  
 Val Met Met Cys Ile Ala Cys Arg Gly Leu Thr Pro Asp Asp Ser Asn  
 195 200 205  
 Phe Lys Ala Val Ser Tyr His Ala Ser Gly Gln Asn Val Ala Tyr Arg  
 210 215 220  
 Pro Gly Gly Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Arg Asn  
 225 230 235 240  
 Lys Lys Ile Tyr Asp Gly Gly Ala Arg Thr Glu Asp Asp Glu Gln Ser  
 245 250 255  
 His Pro Thr Lys Tyr Asp Tyr Val  
 260

<210> 65  
 <211> 132  
 <212> PRT  
 <213> Mouse

<400> 65  
 Ala His Pro Arg Pro Gly Ala Arg Arg Pro Arg Leu Leu Ala Phe Gln  
 1 5 10 15  
 Ala Ser Cys Ala Pro Ala Pro Gly Ser Arg Asp Arg Cys Pro Glu Glu  
 20 25 30  
 Gly Gly Pro Arg Cys Leu Arg Val Tyr Ala Gly Leu Ile Gly Thr Val  
 35 40 45  
 Val Thr Pro Asn Tyr Leu Asp Asn Val Ser Ala Arg Val Ala Pro Trp  
 50 55 60  
 Cys Gly Cys Ala Ala Ser Gly Asn Arg Arg Glu Cys Glu Ala Phe  
 65 70 75 80  
 Arg Lys Leu Phe Thr Arg Asn Pro Cys Leu Asp Gly Ala Ile Gln Ala  
 85 90 95  
 Phe Asp Ser Leu Gln Pro Ser Val Leu Gln Asp Gln Thr Ala Gly Cys  
 100 105 110  
 Cys Phe Pro Arg Val Ser Trp Leu Tyr Ala Leu Thr Ala Leu Ala Leu  
 115 120 125  
 Gln Ala Leu Leu  
 130

<210> 66  
 <211> 764  
 <212> DNA  
 <213> Mouse

<400> 66  
 gcagcaccga gcgccaagcg caccaggcac cgcgacagac ggcaggagca cccatcgacg 60  
 ggcgtactgg agcgagccga gcagagcaga gagaggcgtg cttgaaaccg agaaccaagc 120  
 cgggcgccat cccccggcgc ccgcacgcac aggcgcggcg cctccttgcc tccctgctcc 180  
 ccaccgcgcc cctccggcca gcatgaggct cctggcggcc gcgctgctcc tgetgctcct 240  
 ggcgctgtgc gcctcgcgcg tggacgggtc caagtgtgtaag tgttcccgga aggggcccga 300

```

gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccac actgcgagga 360
gaagatgggt atcgtcacca ccaagagcat gtccaggtag cggggccagg agcactgcct 420
gcaccctaag ctgcagagca ccaaagcgtt catcaagtgg tacaatgcct ggaacgagaa 480
gcgcagggtc tacgaagaat aggggtggacg atcatggaaa gaaaaactcc aggccagttg 540
agagacttca gcagaggact ttgcagatta aaataaaagc cttttctttc tcacaagcat 600
aagacaaatt atatattgct atgaagctct tcttaccagg gtcagttttt acattttata 660
gctgtgtgtg aaaggcttcc agatgtgaga tccagctcgc ctgcgcacca gacttcatta 720
caagtggctt tttgctgggc ggttggcggg gggcgggggg acct 764

```

<210> 67  
 <211> 288  
 <212> DNA  
 <213> Human

```

<400> 67
gcggccgcgc tgctcctgct gctgctggcg ctgtacaccg cgcgtgtgga cgggtccaaa 60
tgcaagtgtc cccggaaggg acccaagatc cgctacagcg acgtgaagaa gctggaaatg 120
aagccaaagt acccgactg cgaggagaag atggttatca tcaccaccaa gagcgtgtcc 180
aggtaccgag gtcaggagca ctgcctgcac cccaagctgc agagcaccaa gcgcttcac 240
aagtgttaca acgcctggaa cgagaagcgc aggggtctacg aagaatag 288

```

<210> 68  
 <211> 95  
 <212> PRT  
 <213> Human

```

<400> 68
Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala Arg Val
1 5 10 15
Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr
20 25 30
Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu
35 40 45
Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly
50 55 60
Gln Glu His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile
65 70 75 80
Lys Trp Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
85 90 95

```

<210> 69  
 <211> 234  
 <212> DNA  
 <213> Mouse

```

<400> 69
tccaagtgtg agtggtcccg gaagggggccc aagatccgct acagcgacgt gaagaagctg 60
gaaatgaagc caaagtaccc aactgcgag gagaagatgg ttatcgtcac caccaagagc 120
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<210> 70  
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 <212> PRT  
 <213> Mouse

<400> 70

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Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
      20           25           30
Met Val Ile Val Thr Thr Lys Ser Met Ser Arg Tyr Arg Gly Gln Glu
      35           40           45
His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
      50           55           60
Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
65           70           75

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gtgtccaggt accgaggtca ggagcactgc ctgcacccca agctgcagag caccaagcgc      180
ttcatcaagt ggtacaacgc ctggaacgag aagcgcaggg tctacgaaga atag          234

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<210> 72  
 <211> 77  
 <212> PRT  
 <213> Human

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<400> 72
Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys Ile Arg Tyr Ser Asp
 1           5           10           15
Val Lys Lys Leu Glu Met Lys Pro Lys Tyr Pro His Cys Glu Glu Lys
      20           25           30
Met Val Ile Ile Thr Thr Lys Ser Val Ser Arg Tyr Arg Gly Gln Glu
      35           40           45
His Cys Leu His Pro Lys Leu Gln Ser Thr Lys Arg Phe Ile Lys Trp
      50           55           60
Tyr Asn Ala Trp Asn Glu Lys Arg Arg Val Tyr Glu Glu
65           70           75

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 <213> Pinus radiata

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&lt;210&gt; 74

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Eucalyptus grandis

&lt;400&gt; 74

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tct						363

# INTERNATIONAL SEARCH REPORT

International application No.  
**PCT/NZ00/00256**

## A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. <sup>7</sup>: C12N 15/11

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

SEE ELECTRONIC DATA BASES

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

SEE ELECTRONIC DATA BASES

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EMBL, GenBank, PIR, GenePept: Sequence IDs 1, 36, 2, 37, 3, 38, 4, 39, 5, 40

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenBank Accession No. AL034558 28 July 1999 Whole Sequence w.r.t. Sequence ID 3	1 - 14
X	GenPept Accession No. CAA29045 21 March 1995 Whole Sequence Frame +2 w.r.t. Sequence ID 4	1 - 14
X	GenBank Accession No. AR018857 5 December 1998 & US 5783182 Whole Sequence w.r.t. Sequence ID 5	1 - 14

☒ Further documents are listed in the continuation of Box C ☒ See patent family annex

<p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p>		<p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&amp;" document member of the same patent family</p>
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Date of the actual completion of the international search <b>28 March 2001</b>	Date of mailing of the international search report <b>29.03.2001</b>
Name and mailing address of the ISA/AU  AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustrialia.gov.au Facsimile No. (02) 6285 3929	Authorized officer  <b>CRAIG ALLATT</b> Telephone No : (02) 6283 2414

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ00/00256

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GenPept Accession No. CAB40181 14 December 1999 Whole Sequence w.r.t. Sequence ID 40	1 - 14

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ00/00256

## Box I Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☐ Claims Nos :  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
  
3. ☐ Claims Nos :  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

## Box II Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See Supplemental Box

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  
Claims 1 - 14 partially.(See Supplemental Box)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/NZ00/00256

### Supplemental Box

(To be used when the space in any of Boxes I to VIII is not sufficient)

#### Continuation of Box No: II

In the present application, the feature that all sequences come from "mammalian sources" does not provide a special technical feature. Genes and their expressed proteins from "mammalian sources" have been sequenced. Cells from "mammalian sources" comprise a variety of different animals and cell types. Moreover the applicant has provided no evidence that the nucleotide sequences of the present application, and the peptides they express, form a unique group of protein types. On the contrary, putative peptides derived from the nucleotide sequences of the application have functions assigned on the basis of their similarity to known proteins expressed by a variety of cell types.

The applicant has grouped the polynucleotides of the application into activity categories according to putative functions of the proteins they encode. However, most of the applicants' groupings do not form a homogenous set of proteins either in structure or function. Moreover, it is noted that most of the peptides encoded by the polynucleotides are assigned to more than one activity category.

The ISA considers that each nucleotide/peptide sequence pair (defined in Table 1 pages 8 - 19) comprises one invention and that there are 35 different inventions (the inventions being numbered sequentially).

However, as a service to the applicants, the ISA will search the first five inventions without inviting additional search fees.

Therefore the ISA has searched SEQ IDs 1, 36, 2, 37, 3, 38, 4, 39, 5, and 40.



### Information on patent family members

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report				Patent Family Member			
US	5783182	AU	11609/97	CA	2237929	EP	870057
		WO	9718454				
END OF ANNEX							